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Estimation of the relative contribution of different food and animal sources to human Salmonella infections in the European Union[1]

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ABSTRACT

EU Member States are required to collect, evaluate and report data on zoonoses, zoonotic agents, antimicrobial resistance and food-borne outbreaks to the European Commission each year. EFSA is responsible for examining, analyzing and summarizing these data, and for publishing the results in the Community Summary Report. The identification of sources of human infections is one of the key analyses in the Community Summary Report. This report provides estimates on the relative contribution of different food and animal sources to human *Salmonella* infections in the European Union, European regions and Member States. Two approaches to attribute human *Salmonella* infections to the responsible food-animal sources were applied. Data used in the models covered the period from 2006 to 2009. The results of the microbial subtyping model showed that the relative contribution of food-animal sources varied between regions and countries. The laying hen reservoir was estimated to be the most important source in the EU contributing with 43.8% (95% Credibility Interval (CI) 43.2 – 44.4%) of cases attributed to this source, followed by pigs (26.9%, 95% CI 26.3-27.6%). Turkeys and broilers were estimated to be less important sources of *Salmonella*, contributing with 4.0% (95% CI 3.8-4.3%) and 3.4% (95% CI 3.1-3.7%), respectively. A total of 9.2% of all salmonellosis cases were reported as being travel-related, and 3.6% of cases were reported as being part of outbreaks with unknown source. Nine percent of cases could not be attributed to any source included in the model. The results of an analysis of data from outbreak investigations attributed salmonellosis to 19 food sources and water. Eggs were estimated to be the most important source of disease in the study period, followed by pork, chicken, the general category "meat and poultry", and dairy products. An analysis by year using data from 2007-2009 showed that the contribution of eggs decreased in 2009, and the proportion of disease attributed to other sources varied over the years and between regions. The report discusses assumptions and limitations of the two approaches and concludes with a number of recommendations.

[1] **(Question No EFSA-Q-2010-00685). Accepted for Publication on 28 July 2011.**

SUMMARY

Salmonella spp. is one of the most common and widely distributed foodborne pathogens in the European Union. Surveillance programmes and intervention strategies to control foodborne salmonellosis have been implemented in EU Member States, but a precise evaluation of the effect of such interventions is difficult, partly due to the lack of information of the public-health impact of specific sources on the incidence of foodborne infections. To identify and prioritize effective food safety interventions, it is essential to quantify the contribution of important food sources to the burden of human salmonellosis.

In this report, two methods to attribute human *Salmonella* infections to the responsible food-animal sources in the EU were applied, specifically a microbial subtyping approach and an analysis of data from outbreak investigations. Human *Salmonella* infections reported to the European Centre for Disease Prevention and Control (ECDC), *Salmonella* serovar data collected as part of the EU-wide Baseline Surveys (BS) conducted in the period from 2005-2008, and data reported by the EU Member States in 2005-2009 including foodborne disease outbreaks published in the Community Summary Reports (CSRs) were available for analysis. After a careful descriptive analysis, data were selected and analysed to make inferences about the most important sources of human salmonellosis in the EU, as well as to highlight regional differences.

The microbial subtyping model for source attribution was applied to data from 24 Member States (MSs) and attributed human sporadic salmonellosis to four animal reservoirs: pigs, broilers, layers and turkeys. In order to account for the trade of food between MSs, food production and trade data extracted from EUROSTAT were used to estimate the amount available for consumption of each food source in each MSs. Results are presented for the whole of EU, and by the MS reporting the human salmonellosis cases. Results showed that the relative contribution of food-animal sources varied between regions and countries. The laying hen reservoir was estimated to be the most important source in the EU, contributing with 43.8% (95% Credibility Interval (CI) 43.2 – 44.4%) of cases attributed to this source, followed by pigs (26.9%, 95% CI 26.3-27.6%). Turkeys and broilers were estimated to be less important sources of *Salmonella*, contributing with 4.0% (95% CI 3.8-4.3%) and 3.4% (95% CI 3.1-3.7%), respectively. A total of 9.2% of all salmonellosis cases were reported as being travel-related, and 3.6% of cases were reported as being part of outbreaks with unknown source. Nine percent of cases could not be attributed to any source included in the model.

A regional analysis showed that layers were the most important source in Northern, Eastern and Western Europe, with between 30.0% and 57.6% of the *Salmonella* reported cases attributed to this source, whereas pigs were the major source of salmonellosis in Southern Europe, contributing with 43.6% of the cases. Turkeys and broilers contributed with varying but lower proportions of reported cases. A large proportion of the reported *Salmonella* infections in Northern European countries were acquired abroad.

Data availability and quality varied substantially between countries. Particularly the variation in the human surveillance systems in place in the countries and the different levels of serovar details

reported in both humans and food-animal sources are assessed to contribute to the uncertainty of the results of the source attribution model based on subtyping. In addition, some reservoirs of *Salmonella* (e.g. cattle/beef) were not included in the model due to lack of data or poor data quality. The possible consequences of this are discussed. The report concludes with a number of recommendations to improve the data quality and availability for future source attribution studies.

The analysis of data from outbreak investigations included data from 27 MSs, Norway and Switzerland and attributed salmonellosis to 19 food sources and water. Eggs were estimated to be the most important source of disease in the study period, followed by pork, chicken, the general category "meat and poultry", and dairy products. An analysis by year showed that the contribution of eggs decreased in 2009, and the proportion of disease attributed to remaining sources varied over the years and between regions.

Limitations of the use of outbreak data for attribution of foodborne disease in general are recognized and linked to the fact that outbreaks may not be representative of all human cases occurring in the population, and that certain food vehicles are more likely to be associated with reported outbreaks than others, which can lead to an overestimation of the proportion of human illness attributed to a specific food.

For both source attribution models, the estimated differences in the relative importance of sources may be a consequence of differences i) in the epidemiology of *Salmonella* in EU Member States, i.e. the *Salmonella* occurrence (prevalence and numbers) in food-animal sources, ii) in food consumption and preparation patterns, iii) in animal and food production systems, or iv) in the efficiency of surveillance programmes in place.

The two source attribution methods applied attribute human illness at different points in the farm-to-consumption continuum, have different data requirements and data availability, and utilize different statistical methods. As a consequence, the methods are able to address different public health questions and to inform risk management strategies at different points in the food production chain. Thus, comparisons of results should be made with care since the two approaches are not necessarily expected to give the same results.

Despite data limitations and the resulting uncertainty in the results, the obtained source attribution estimates are considered useful for delineating risk management strategies. These represent the first indication of which animal-food sources are most important for human salmonellosis in several countries, and highlight regional differences in the contribution of different food-animal sources for disease and on the effect of surveillance and control programmes in place in EU Member States.

Key words: *Salmonella*, source attribution, foodborne, outbreaks, *Salmonella* surveillance and control

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BACKGROUND

The European Community system for monitoring and collection of information on zoonoses and antimicrobial resistance is established by Directive 2003/99/EC on the monitoring of zoonoses and zoonotic agents[2]. This Directive requires the Member States to collect, evaluate and report data on zoonoses, zoonotic agents, antimicrobial resistance and food-borne outbreaks to the European Commission each year. The system used is based on that of the Member States, and in a few cases it is harmonized by the Community legislation to the extent that the results from the monitoring are directly comparable between the Member States.

The Member States have to send their report on to the European Commission each year by 31st May. The Commission shall submit this information to the European Food Safety Authority (EFSA), who is responsible for examining the data and for publishing the Community Summary Report from the results. The report is prepared in collaboration with the European Centre for Disease Prevention and Control (ECDC) and EFSA's Zoonoses Collaboration Centre. In practice Member States report the information on zoonotic agents in animals and food through a web-based reporting application run by EFSA. The latest Community Summary Report on zoonoses is from the reporting year 2009 (EFSA, 2011a). In the Community Summary Report on zoonoses, the information received from the Member States is analysed and summarised specifically to identify trends in the occurrence of the zoonotic agents and the sources of human infections.

Member States are also required to submit annual data on *Salmonella*. Substantial quantity of information on the *Salmonella* serovars and phage types isolated from different foodstuffs and animal species are received each year. Additional data on serovars and phagetypes of *Salmonella* is available from the Community-wide baseline surveys that are coordinated by the Commission and analysed by EFSA. The analyses reports are available on EFSA website at http://www.efsa.europa.eu/en/zoonoses/zoonosesscdocs.htm.

Data on zoonoses cases in humans are provided through the Community networks for the epidemiological surveillance and control of communicable diseases established under Decision No 2119/98/EC run by ECDC[3]. Human salmonellosis data is reported to the European Surveillance System (TESSy) in ECDC and aggregated results are also presented in the Community Summary Reports on Zoonoses.

The ability to attribute cases of human disease to specific reservoirs, food vehicles or other responsible sources is recognised as critical for the identification and prioritisation of food safety interventions. Efforts to quantify the importance of specific sources for human illness are gathered under the term "source attribution" or "human illness source attribution" and can be

[2] Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC (OJ L 325, 12.12.2003 p. 31)

[3] Regulation 851/2004/EC of the European Parliament and of the Council of 21 april 2004 establishing a European Centre for disease prevention and control

defined as the process of determining the proportion of a particular disease that is acquired from a given source (e.g. chicken) and potentially through a given pathway (e.g. food or direct animal contact). Several methods for source attribution have been described, including microbiological approaches, epidemiological approaches, intervention studies and expert elicitations (Pires et al., 2009; EFSA, 2008a; EFSA, 2010f).

TERMS OF REFERENCE

The overall objective of the contract resulting from the present procurement procedure is to conduct a source attribution analysis to investigate the importance of different food categories and animal populations as the source of *Salmonella* infections in humans in the European Community.

The specific objectives of the contract resulting from the present procurement procedure are as follows:

- to analyse in detail data on *Salmonella* serovars and phage types isolated from humans and reported under the Decision No 2119/98/EC to the ECDC as complemented by Decision 2000/96/EC[4] with amendment 2003/542/EC[5]
- to estimate the relative contribution of different food and animal sources to human *Salmonella* infections in the European Union and European regions.

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Contract title: Estimation of the relative contribution of different food and animal sources to human *Salmonella* infections in the European Union.

Contract number: CT/EFSA/Zoonoses/2010/02

4 Decision 2000/96/EC on communicable diseases to be progressively covered by the EU network under Decision No 2119/98/EC of the European Parliament and of the Council, OJ L 180, 11.7.2009, p. 22–23

5 Decision 2003/542/EC Commission Decision of 17 July 2003 amending Decision 2000/96/EC as regards the operation of dedicated surveillance networks, OJ L 185, 24.7.2003, p. 55–58

1. Introduction

Foodborne diseases are a major public-health concern worldwide. The burden of pathogens commonly transmitted through foods has increased substantially in the last decades (Greger, 2007), and the World Health Organization (WHO) estimates that up to one third of the population each year suffers from a foodborne infection (WHO, 2005). This global rise has been associated with an increase in the consumption of products of animal origin, with the implementation of methods of intensive production required to supply such a demand, and with the globalization of food trade. Changes in consumption patterns and international travel have also promoted the potential spread of pathogens formerly uncommon or unknown in specific world regions.

The economic, social and public-health importance of these diseases has motivated many countries to implement surveillance and intervention strategies to control foodborne illnesses, particularly foodborne zoonoses (Wegener et al., 2003; EFSA, 2009). However, a precise evaluation of the effect of such interventions is difficult, partly due to the lack of information of the public-health impact of specific sources on the incidence of foodborne infections. To identify and prioritize effective food safety interventions, it is essential to quantify the contribution of important sources of foodborne pathogens to the burden of human illness.

A variety of methods to attribute foodborne diseases to specific sources are available, including approaches based on analysis of data from microbiological and epidemiological studies, intervention studies, and expert elicitations. Source attribution methods present different advantages and limitations, and their applicability depends on the pathogen in question and on the data available to address a specific public health question (Pires et al., 2009; EFSA, 2008a).

Salmonella spp. is one of the most common and widely distributed foodborne pathogens in the European Union (EFSA, 2008a). *S.* Enteritidis and *S.* Typhimurium are the most frequently reported serovars, but a wide range of other serovars frequently cause disease in humans and thus are of public health significance (Vieira *et al*., 2008; EFSA, 2010a). Human infection is most often foodborne, but other routes of infection, namely contact with live animals and environmental transmission, have been identified (Baker et al., 2007; O'Reilly et al., 2007).

Several *Salmonella* source attribution studies have been conducted worldwide, including in European countries (e.g. Denmark: Hald et al., 2004; Pires et al., 2010a; Sweden: Whalström et al., *in press;* the Netherlands: Valkenburgh et al., 2007). These studies were conducted in countries with well-established public health and animal surveillance systems that assure the existence of representative data for source attribution and epidemiological analyses. Thus far, the relative contribution of different food sources for human salmonellosis in remaining countries within Europe had not been assessed. An exception is an analysis of outbreak data for source attribution of salmonellosis in the European Union (Pires et al., 2010b), which results suggested regional differences in the relative importance of food sources for disease, but also reflected the variability in the effectiveness of implemented surveillance systems and quality of data in different countries, the latter preventing any direct comparison of the public health impact of food sources between EU countries or regions.

In this report, human *Salmonella* infections reported to the European Surveillance System (TESSy) at the European Centre for Disease Prevention and Control (ECDC), *Salmonella* serovar data collected as part of the EU-wide Baseline Surveys (BS) conducted in the period from 2005-2008, data reported by the EU Member States (MSs) in 2005-2008 published in the Community Summary Reports (CSRs), and food production and trade data as summarized by EUROSTAT were available and analysed to make inferences about the most important sources of human salmonellosis in EU, as well as to highlight regional differences. Two source attribution methods were applied, specifically a microbial subtyping approach and an analysis of data from outbreak investigations.

2. Objectives

The objective of this study was to estimate the relative contribution of different food sources for the burden of human salmonellosis in the European Union (EU) by

1) Developing an EU-wide source attribution model based on microbial subtyping
2) Updating an existing EU source attribution model based on foodborne outbreak data.

In order to do this, a thorough analysis of all relevant and available human and animal-food data was performed and the results are presented in the appendices of this report.

3. Materials and methods

Two source attribution approaches were used to estimate the relative importance of food sources for human *Salmonella* infections in the EU: 1) a Bayesian modelling approach based on microbial subtyping data and 2) an analysis of data from foodborne disease outbreak investigations. The two methods have distinct data requirements and attribute human illness at different points of the food chain. While the latter uses data on food sources implicated in reported foodborne outbreaks and thereby represents attribution at the point of exposure to the food item, the microbial subtyping approach uses monitoring or survey data from the food-animal sources and consequently attributes human cases to the original reservoir of *Salmonella*. A more detailed explanation of differences between source attribution methods can be found in Pires et al. (2009) and EFSA (2008a).

3.1. Source attribution analysis based on microbial subtyping

The principle of the source attribution approach by microbial subtyping is to compare the number of human cases caused by different subtypes of the foodborne pathogen with the distribution of the same subtypes in different food-animal sources (Pires et al., 2009). Typing schemes are applied to distinguish between strains or isolates of a pathogen (Pagotto and Reid, 2011). The approach utilizes a collection of temporally and spatially related isolates from multiple sources

and humans, and thus is facilitated by the existence of surveillance programmes that focus on the collection of isolates from the major sources of disease.

In this study, the model was built in Bayesian framework on the basis of the method described by Hald *et al.* (2004) and extended by Pires & Hald (2010), where *Salmonella* subtype distributions in animals in a given country are compared with the subtype distribution in humans in the same country. The objective is to estimate the number of reported human cases that can be attributed to each source based on the observed surveillance data. The model was adapted to accommodate data from multiple countries, thereby adding a third dimension to the original model (in addition to subtype and source-related factors) and was based on the distribution of serovars in humans and food-animal source, since insufficient additional subtyping information was available for the majority of the data.

3.1.1. Data requirements

The model attributes human sporadic and domestic *Salmonella* infections to specific food-animal sources in each country based on 1) the number of laboratory-confirmed infections caused by each *Salmonella* serovar, including possible outbreak or travel information for each case, 2) prevalence of each serovar in the different sources, and 3) amount of food source available for consumption in each country broken down by the country of origin. Prevalence data representing the food-animal source at the reservoir level are preferred (Pires *et al*., 2009).

A sporadic case is defined as a subject that could not be associated with a recognized foodborne disease outbreak. To avoid possible overestimations of the number of cases attributed to each source due to the inclusion of large outbreaks associated with one specific source, only sporadic cases was included in the model. Sporadic cases are defined as cases not reported as being part of outbreaks and are estimated as the total number of reported cases per serovar minus the number of outbreak-related cases per serovar. It is assumed that one outbreak contributes (counts) with one sporadic case. Outbreak-related cases are added to the final results of the model and attributed either to the source implicated in the outbreak (if the outbreak was investigated and the responsible source identified and reported) or to outbreaks with *unknown source*. A domestic case is defined as a subject with no history of foreign travel reported before the disease onset.

3.1.2. Data availability and data selection

Salmonella data from food-animal sources, public health surveillance data and production and trade data were available from multiple sources. All utilized data covered the period between 2007 and 2009. Data on the prevalence of *Salmonella* serovars in animals and food were available from the EU BS conducted in different animal species (EFSA, 2007b; EFSA 2007d; EFSA 2008b, EFSA, 2010c) and from the CSRs as published by the European Food Safety Authority (EFSA) from 2006 to 2009. Data on reported human *Salmonella* infections was provided by ECDC through EFSA. These data included both case-based and aggregated data and

were complemented with other data sources (e.g. national monitoring or laboratory surveillance data not published in the CSRs) when necessary and possible. EU animal-food production and trade data were available from EUROSTAT published statistics. Data were stored and analyzed in SAS Enterprise Guide, SAS Institute, SAS/STAT® User's Guide, Version 8, Cary, NC: SAS Institute Inc., 1999.

Data origin and countries providing information for each food-animal reservoir, reported human cases and cases related to foodborne *Salmonella* outbreaks are summarized in Appendix A. An overview of data analysed in order to construct the dataset for the source attribution model is shown in Appendix B. A complete descriptive analysis of the human *Salmonella* incidence and food-animal *Salmonella* prevalence data can be found in Appendix C. The appendices describe reported *Salmonella* monitoring data as available from all countries, humans and the five main animal reservoirs, regardless of their final use in the source attribution model.

3.1.2.1. Reported cases of human salmonellosis

The overall reported incidence of human salmonellosis decreased from 2007 to 2009, which is mainly explained by a decline in the number of reported *S.* Enteritidis cases (EFSA, 2011a). In contrast, reported cases of *S.* Typhimurium increased with around 40% from 2007 to 2008, whereas a decrease of 18% was observed from 2008 to 2009. *S.* Enteritidis and *S.* Typhimurium remained the most frequently reported serovars constituting around 75% of all confirmed cases (Table 1). Remaining cases were associated with a variety of serovars with *S.* Infantis being the most common (1.6% of all confirmed cases in 2009) and the rest not individually exceeding 1%. Between 6,613 and 17,359 *Salmonella* isolates were of "unknown" serovar. This group includes untyped isolates, where no typing was attempted and untypeable isolates, where typing was attempted but outcome was not successful. It should further be noted that the reported human data in Table 1 represent aggregated data and in some cases serovars reported individually in one year may be reported in the group "Other" in previous years.

Table 1. Reported and confirmed cases of human salmonellosis in the EU, 2007-2009. Source: CSR (EFSA 2010a, EFSA 2011a)

	Reporting year					
	2009 (N=26 MSs)		2008 (N=26 MSs + 3 non-EU)		2007 (N=26 MSs + 3 non-EU)	
Serovar	N	%	N	%	N	%
S. Enteritidis	53,382	52.3	70,091	58	81,472	64.5
S. Typhimurium	23,759	23.3	26,423	21.9	20,781	16.5
S. Infantis	1,616	1.6	1,317	1.1	1,310	1
S. Bovismorbificans	433	0.4	501	0.4	-	-
S. Hadar	507	0.5	-	-	479	0.4
S. Virchow	736	0.7	860	0.7	1,068	0.8
S. Derby	671	0.7	624	0.5	469	0.4
S. Newport	760	0.7	787	0.7	733	0.6
S. Stanley	-	-	529	0.4	589	0.5
S. Agona	-	-	636	0.5	387	0.3
S. Kentucky	460	0.5	497	0.4	431	0.3
S. Saintpaul	452	0.4	-	-	-	-
Other	19,225	18.8	18,495	15.3	18,562	14.7
Total	102,001		120,760		126,281	
Unknown	6,613		6,636		9,814	

The reduction in the number of human salmonellosis cases due to *S.* Enteritidis is believed to be a result of an improved surveillance and control of *S.* Enteritidis in breeding hens and in laying hens in many MSs (EFSA, 2011a). In contrast, the increased reported incidence of *S.* Typhimurium infections may indicate that one or more sources of these infections are increasing in importance.

Data on the number and serovar distribution of human cases reported to the TESSy system from 2007 to 2009 were extracted on 6th of July 2010 and provided by ECDC through EFSA. Additional datasets with more detailed serovar information were provided by Poland and Portugal.

The total number of reported cases includes sporadic, travel and outbreak-related infections. Travel-related cases were reported as "imported". Information on imported cases varied in frequency and quality. The proportion of travellers varied greatly among MSs and for some countries such as Sweden and Finland, the travel-related cases represented the majority of all salmonellosis cases and for some MSs (nine in 2009), 100% of the cases were reported to be of "unknown location of origin". Data on domestic versus travel-related cases are, therefore, often incomplete. In the source attribution model, all records with missing or unknown travel information were considered domestically acquired in the reporting country.

Data on foodborne salmonellosis outbreaks were taken from the CSRs. The number of outbreak-related cases per serovar and country were identified and subtracted from the total number of domestically acquired cases to estimate the number of sporadic cases if this was not already done by the reporting country. One outbreak was assumed to contribute with one sporadic case.

Appendix C(b) provides a more detailed analysis of the human data applied in the model.

3.1.2.2. Animal and food data from the EU-wide Baseline Surveys

Data from the EU BS on the prevalence of *Salmonella* in broiler carcasses (2008), slaughter pigs (2006-2007) and fattening turkeys (2006-2007) were used. These datasets were considered to be the most representative of the given reservoir, since no harmonised EU monitoring in pigs and turkeys is currently in place, and the broiler carcass study was considered to provide sufficiently recent data with a better detailing of the serovar distribution when compared to the existing EU monitoring data. Greece did not take part in the 2008 broiler carcasses study, so serovar information in this country was supplied with data from the broiler flocks BS, conducted between 2005 and 2006 (EFSA, 2007b). For slaughter pigs, the results of the lymph node sampling were available for most MSs except Malta and Romania (Appendix A). For turkeys, data from fattening turkeys were used. Estonia, Latvia, Luxembourg and Romania were not part of the turkey BS. Consequently, data on *Salmonella* serovars in turkeys from these countries were provided by CSR data from 2006 and 2008 (EFSA, 2007a; EFSA, 2010a) except for Romania, where no data were available.

3.1.2.3. Animal and food data from the annual EU monitoring

Data for laying hens and cattle were collected from the CSRs published by EFSA in different years. Data on *Salmonella* serovars in laying hens were obtained from the CSR 2008 (EFSA, 2010a), which was the first year of harmonised reporting. Data from the laying hens BS were not considered because this study was conducted between 2004 and 2005, and it is expected that the implementation of the Commission Regulation (EC) No 1168/2006 for laying hens flocks of *Gallus gallus* has resulted in significant changes in the *Salmonella* serovar prevalences in this reservoir in many MSs. Data were selected according to the recommendations found in EFSA (2010d). Cattle data was retrieved from the CSR 2007, 2008 and 2009 (EFSA, 2009; EFSA, 2010a; EFSA, 2011a). No data from Cyprus or Malta were identified, and for some countries only a single year of data were available (Appendix A).

Appendix C(a) provides a more detailed analysis of the food-animal data available.

3.1.2.4. Food production and trade data

Food production data were derived by EFSA from existing EUROSTAT datasets, the EUROSTAT database on slaughtered animals for food consumption (EUROSTAT, 2010c), and the EUROSTAT PRODCOM database (EUROSTAT, 2010d). Data on annual slaughtered animals for meat production for cattle, pigs and poultry (no differentiation between broilers and turkeys) were available for all MSs and all years, except for Belgian poultry meat production for 2007 and 2008. Availability of data on the annual quantities of poultry, pork and bovine meat and eggs produced varied per year and per MS. For example, egg production data were lacking for several countries, and data for most food sources and most years were missing in some countries (e.g. Cyprus). Missing data on annual quantities of poultry meat products sold per MS, with differentiation between boilers, turkeys and other poultry species were obtain from the 2009 annual report of the Association of Poultry Processors and Poultry Trade in the EU Countries (AVEC, 2009).

Data on the import and export of broiler meat, turkey meat, pig meat, beef and eggs for 2007, 2008 and 2009 were derived by EFSA from existing EUROSTAT datasets (EUROSTAT, 2010a). International trade statistics, as produced by EUROSTAT, report the value and quantity of goods traded between EU MSs (Intrastat) and by EU MSs with third countries (Extrastat). European Community legislation ensures that the statistics provided to EUROSTAT by the MSs are based on legal texts and on harmonized definitions and procedures. However, an evaluation of the quality of the trade data collected by EUROSTAT has revealed major and persistent inconsistencies in the various MSs intra-EU trade statistics (EFSA, 2010b). In this report, extra-EU food trade was not considered. Data on the export of the food sources included in this study to other MSs were available for all considered countries with the exception of the amount of eggs exported from Cyprus. All MSs reported imports from other MSs for all food products in the study period.

In order to consider the intra-community trade of food between the MSs and the impact of this trade on the incidence of human salmonellosis in importing countries, the amount available for consumption of each food source in a given MS was estimated as the total production minus the export plus the import. The resulting trade matrix for each food source indicating the quantity transferred from an exporting to an importing country was used as input to the model.

3.1.3. Data management

3.1.3.1. Animal data reported by EU Member States and EU Baseline Surveys

Positivity percentages of *Salmonella* serovars in the different food-animal sources were calculated to describe the available data. Because analysed data originated from two different sources, the CSRs and the BSs, positivity percentages calculated from the raw data were preferred to prevalence data to facilitate comparisons despite differences in sample sizes, study designs and animal populations. This approach did not influence source attribution estimates, since those are based on the relative proportion of serovars within each source and country. The

positivity percentages were calculated by dividing the number of positive units (samples or herds/flocks) by the number of tested units and multiplying the result by one hundred. To estimate relative frequencies, the numerator was the number of units positive for a specific serovar and the denominator was the number of positive units.

Particularly for the data reported for the CSRs, the serovar information differed between countries with regards to the level of detail reported. In the laying hens dataset, aggregated data or isolates with no serotyping information (e.g. isolates reported as "Other serovars") were redistributed according to presence and proportions of serovars observed in the laying hens BS (EFSA, 2007c). Data from the cattle reservoir were in general poor, and efforts to improve the dataset (include the largest amount of countries possible in the dataset, which implied completing data from Latvia, Lithuania, Slovenia and Denmark with data from the years of 2007, 2006, 2008 and with slaughterhouse carcass samples from 2008, respectively) did not prove sufficient to obtain a representative dataset for this source in the model.

For BS data, no reference for reassigning of serogroups or incomplete identifications was available, and thus isolates were redistributed according to the proportions found among serovar isolates in the same dataset. Study design, sampling schemes and data collection methods can be found in the respective BS reports (EFSA, 2007b; EFSA, 2007d; EFSA, 2008b; EFSA 2010c).

3.1.3.2. Human data

Reported human isolates that were not classified up to serovar level or in which data were reported in aggregated form were reassigned to specific serovars according to proportions observed in previous studies, in the same dataset or in other references. Isolates classified as serogroups were distributed among serovars pertaining to those serogroups, in accordance with the Kauffman-White-Le Minor Scheme 9th edition (WHOCC-Salm, 2007). Isolates classified as "*Salmonella*, serovar unknown", *Salmonella* Subspecies I, *Salmonella enterica ssp. enterica*, *Salmonella* spp. or "*Salmonella* spp., unspecified" were distributed among all serovars observed in the reference documents or datasets, also using the appropriate proportions. When some serovars were specifically reported and others were aggregated as "Others", the aggregated numbers were reassigned to serovars not specified in the original data, following the distributions observed in the reference documents or datasets. The main reference dataset used for this reassignment was the WHO Global Foodborne Infections Network (GFN) Country Databank (CDB), which contains the 15 most commonly identified *Salmonella* serovars among human and non-human sources in 84 countries (http://thor.dfvf.dk/gss). The relative serovar proportions observed in this dataset were used to redistribute records aggregated as "Others". Isolates identified as *S*.1,4,[5],12:i:- or *S*.4,[5],12:i:- were reassigned to *S*. Typhimurium (EFSA, 2010e). Outbreak-related cases were reassigned using the proportions observed in the same dataset, because some serovars may be more prone to generate outbreaks than others, and thus the proportions observed in reported cases may not apply.

3.1.4. Final data used in the model

Based on data availability and quality, four food-animal sources were included in the final model:

- Broilers
- Pigs
- Turkeys
- Laying hens (i.e. eggs)

Since neither harmonised EU monitoring data nor BS data were available for the cattle reservoir, this source was excluded from the final model due to poor data quality, which significantly compromised the validity of the model results when included. The possible consequences of omitting this reservoir are discussed in later sections.

Based on data availability and quality, the following 24 countries were included in model:

- Austria
- Belgium
- Cyprus
- Czech Republic
- Denmark
- Estonia
- Finland
- France
- Germany
- Greece
- Hungary
- Ireland
- Italy
- Latvia
- Lithuania
- Luxembourg
- Poland
- Portugal
- Slovakia
- Slovenia
- Spain
- Sweden
- The Netherlands
- United Kingdom

Twenty-two serovars were selected to be specifically addressed, based on their presence and importance in humans and in the main animal reservoirs in a five-year period:

- *S.* Agona
- *S.* Anatum
- *S.* Bovismorbificans
- *S.* Braenderup
- *S.* Brandenburg
- *S.* Bredeney
- *S.* Derby
- *S.* Enteritidis
- *S.* Hadar
- *S.* Heidelberg
- *S.* Infantis
- *S.* Kentucky
- *S.* Kottbus
- *S.* Livingstone
- *S.* London
- *S.* Mbandaka
- *S.* Montevideo
- *S.* Newport
- *S.* Rissen
- *S.* Saintpaul
- *S.* Typhimurium
- *S.* Virchow

Despite their public health importance in the majority of considered countries, the serovars *S.* Dublin, *S.* Ohio and *S.* Stanley were not included in the list because they were not isolated from the animal sources considered in the source attribution model. Serovars not included in the above list were aggregated as "Others".

3.1.5. Model overview

3.1.5.1. Model parameters

The model estimates the number of cases of sporadic salmonellosis attributed to each source per country and the relative impact of a set of unknown factors. These factors were included as multi-parameter priors and they account for the differences in the ability of different subtypes to cause disease and of different sources to act as vehicles for infection. Multiple loops were included to accommodate data from the 24 countries. The model parameters are presented in Table 2.

Table 2. Parameters used to estimate the number of sporadic cases of salmonellosis attributable to the animal sources

Notation	Description	Estimation
i (1-22)	*Salmonella* serovar	-
j (1-4)	Food-animal source	
c (1-24)	Country where the human case was reported	
k (1-24)	Country of origin of the food product[(a)]	
o_{ci}	Observed cases caused by serovar *i* in country c	Data
ob_{ci}	Observed cases caused by serovar *i* known to be outbreak related in country c. For each outbreak, one case was subtracted so that one outbreak contributed with one sporadic case.	Data
ytc_i	Observed cases caused by serovar *i* in country c that was reported as travel-related	Data
pk_{ji}	Prevalence of serovar *i* in source *j* in country *k*	Data
m_{ckj}	Amount of source *j* available for consumption in country *c* produced in country *k*[a]	Data
a_{cj}	Source-dependent factor for source *j* and country c	dunif(0,max a_{cj})
q_i	Subtype-dependent factor for serovar *i*	dunif(0,max q_i)
$spdoc_i$	Total number of sporadic cases caused by serovar *i* in country *c*	o_{ci} - yt_{ci} – (ob_{ci} + 1)

(a)If the food is produced and consumed in the same country, c=k

The multi-parameter priors constituted a subtype-dependent factor (q_i) and food-source-dependent factor (a_{cj}) and were defined as uninformative prior distributions (uniform distributions). The amount of food source available for consumption in the country where a *Salmonella* case was reported considered both domestically produced and imported foods (m_{ckj}). To retrieve this value for each source, production, export and import data was used as described in 3.1.2. The prevalence of *Salmonella* serovars in the animal-food sources in the country of origin of the food (p_{kji}), the amount of food source available for consumption in the country, where the infections were reported (m_{ckj}), and the number of reported human cases per type per country (o_{ci}) were applied to update our knowledge on the relative size of the parameters q_i and a_{cj} (equation 1). The subtype-dependent factor was estimated as a one-dimension parameter (q_i), meaning that it is a property of the *Salmonella* serovar and assumed independent of the country of infection. The q_i prior for *S.* Enteritidis was defined as 1, and all q_i values were estimated relatively to this one. q_i describes the differences in the ability of the various *Salmonella* serovars to cause human disease, accounting e.g. for differences in the serovars' survivability throughg the food chain and potential differences in pathogenicity. The food-source-dependent factor (a_{cj}) was assumed to vary between countries, accounting for variability in surveillance systems, variations in sampling schemes and changes in consumption patterns not captured by m_{ckj}. This factor may

also include general variations between sources like the bacterial load/concentration in the food, and processing, handling or preparation practices.

The model was set up to estimate the number of human sporadic and domestic cases attributed to each source per country (λc_{ji}) and the posterior distributions for a_{cj} and q_i, assuming that the observed number of sporadic cases per subtype per country (o_{ci}) is Poisson distributed:

Poisson (o_{ci}) =$\sum \lambda_{ci}$, and

$$\lambda_{ckji} = p_{kij} * m_{ckj} * a_{cj} * q_i \quad \text{(equation 1),}$$

where λ_{ckji} is the expected number of cases per serovar *i* and source *j* reported in country *c* and caused by food produced in country *k*, p_{kij} is the prevalence of serovar *i* in source *j* in country *k*, m_{ckj} is the amount of source *j* available for consumption in country *c* produced in country *k*, a_{cj} is the source-dependent factor for source *j* in country *c*, and q_i is the subtype-dependent factor for serovar *i*.

A Markov Chain Monte Carlo (MCMC) simulation, specifically the Gibbs sampler, was applied to arrive to the posterior distributions for a_{cj} and q_i. Five independent Markov chains of 40,000 iterations were run. For each chain, a different set of starting values for the priors, widely dispersed in the target distribution, were chosen. Convergence was monitored using the methods described by Gelman and Rubin (Gelman and Rubin, 1992) and was considered to have occurred when the variance between the different chains was no larger than the variance within each individual chain, and when the chains had reached a stable level. The model was set up in WinBugs 1.4 (http://www.mrc-bsu.cam.ac.uk/bugs/).

3.1.5.2. Model assumptions

Attribution of human *Salmonella* infections to food-animal sources in the EU on the basis of available data implied a number of assumptions:

- All major food sources of human salmonellosis in EU are included in the model.
- The sampling schemes and data collection of the Baseline Studies, the animal surveillance and monitoring programs, the outbreak reporting system and TESSy generate data that are representative of each food source and country;
- Large *Salmonella* outbreaks in the country were reported;
- If there was no travel information or if it was recorded as "Unknown", the *Salmonella* human infection was acquired in the country where it was reported;

- *Salmonella* serovars distributions are constant during short periods of years; consequently isolates not fully identified can be reassigned to specific serovars following proportions found previously in the same country but using other years of data or data sources;

- The ability of a *Salmonella* serovar to cause infection (as represented by q) is a characteristic of the serovar and independent of time period and country of isolation;

- Surveillance schemes, production systems and food preparation techniques influence the estimated ability of a food source to act as a vehicle for infection, and so source-dependent factor a_{cj} varies from country to country.

- The EUROSTAT production and trade data reflects the true flow of food in EU.

- Food imported into a country is also consumed in that country.

3.1.5.3. Goodness of fit

The predictive ability of the model was assessed by estimating the ratio between the observed *Salmonella* cases (sporadic human cases reported in each country) and the number of cases predicted by the model and attributable to sources in each country. A ratio of one reflects a perfect model fit, whereas a ratio higher than 1 means that the model tends to underestimate the number of cases, and an estimate below 1 refers to an overestimation.

3.2. Source attribution analysis based on data from foodborne outbreak investigations

The applied method was based on Pires *et al.* (2010b) and modified to gain knowledge from information from multiple years. The principle is to attribute human illnesses to food sources on the basis of the number of outbreaks that were caused by each of these foods. For this purpose, implicated foods are classified as simple foods (composed by ingredients that belong to one single category), or complex foods (composed by ingredients that belong to multiple categories), and the ingredients that constitute the complex foods are designated through defined criteria.

3.2.1. Data requirements

The model requires data from foodborne outbreak investigations that specifies the country and year of occurrence, the setting of the outbreak (household or general outbreak; a general outbreak is defined as an outbreak that occurred outside a home), and the food implicated in the outbreak if the investigation was successful in identifying the responsible source.

3.2.2. Data availability

Foodborne outbreak data were provided by EFSA, which is responsible for the collection and analysis of national data on foodborne outbreaks from all the MSs, which are reviewed by the European Centre for Disease Prevention and Control (ECDC) (EFSA, 2007c). Only data from verified outbreaks were used (as defined in EFSA, 2007c). Data from 2005 to 2009 was compiled, but attribution analyses were only produced for the time period between 2007 and 2009. Data from outbreak investigations from 2005 and 2006 were used solely to inform estimates for 2007-2009. Data were organized in a way that each reported outbreak corresponded to an observation in the data set. For each observation, information on the year of occurrence, country, location of the outbreak, and implicated source was included. When any of the fields was incomplete, the parameter was included as *unknown*. Utilized data corresponded to investigations of *Salmonella* verified outbreaks in 29 countries (27 Member States, Norway and Switzerland). No verified outbreak cases were reported by Cyprus, Luxembourg or the United Kingdom in 2007-2009, Ireland in 2009, Norway in 2008-2009 and Portugal in 2007. Table 3 presents the number of verified outbreaks reported by each region in the study period.

Table 3. Number of *Salmonella* verified outbreaks by EU region[(a)], 2005 to 2009.

Region	2005[(b)]	2006[(b)]	2007	2008	2009[(c)]	Total
Eastern Europe	1,202	909	150	173	113	2,547
Northern Europe	143	212	38	33	63	489
Southern Europe	585	456	201	104	56	1,402
Western Europe	1,476	1,554	209	170	136	3,545
Total	3,406	3,131	598	480	368	7,983

(a) EU regions as defined by the United Nations (Pires et al., 2010b). Eastern Europe: Czech Republic, Hungary, Poland and Slovakia. Northern Europe: Denmark, Estonia, Finland, Ireland, Latvia, Lithuania, Sweden and the United Kingdom. Southern Europe: Cyprus, Greece, Italy, Portugal, Slovenia, Spain. Western Europe: Austria, Belgium, France, Germany, Luxembourg and the Netherlands

(b) Data used only to inform estimates for 2007-2009

(c) Data as available by December 2010

3.2.3. Food categorization

Food items were categorized using a hierarchical scheme (Figure 1), adapted from Painter et al. (2009). All foods were divided in three main groups, which were sub-divided in more specific food categories. Uncommon food items were included at a higher level in the more general categories. As an example, four sub-categories were specified within poultry (layers, chicken, ducks and turkey), but this category may also include other poultry types (e.g. goose and doves). Foods that contained only one category (e.g. steak contains beef; salad contains only vegetables, even though it contains multiple vegetables) were considered "simple foods", while foods containing ingredients belonging to different categories (e.g. tiramisù contains eggs, dairy products, grains and sugar) were considered "complex foods". Each implicated food was assigned to one or more mutually exclusive food categories, according to its ingredients. The ingredient list for complex foods' reported outbreaks was obtained by a review of recipes on the

World Wide Web, as described by Painter et al. (2009): the top three recipes from a Google search were selected; when recipes were conflicting, the ingredients listed in at least two of the three recipes were included. Non-reported sources of infection were classified as unknown. Categories belonging to the main group "land animals" were in some cases grouped together in unspecified meat and poultry, depending on the level of detail of information available from the outbreak data.

Water was included as a source in this study, but was not categorized in the overall classification scheme. Water was not included in our definition of food and was considered an environmental route of transmission.

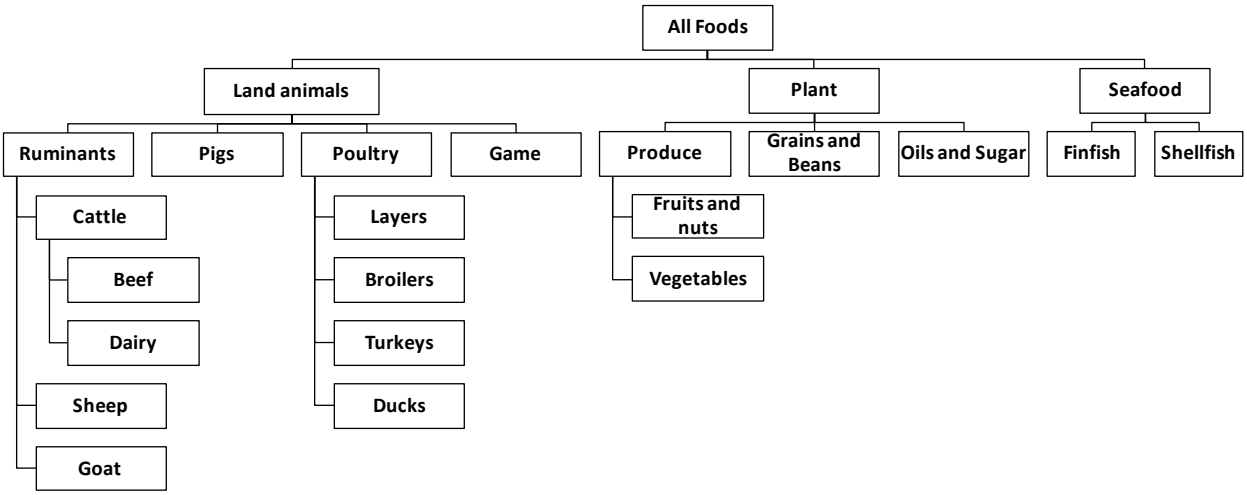

Figure 1: Hierarchical scheme for categorizing food items into commodities.

3.2.4. Model overview

The model parameters are described in Table 4. The proportion of disease that can be attributed to each food source was estimated based on the number of simple-food outbreaks caused by that source, on the ingredients (food categories) composing complex-foods, and on the probability that each of these categories were the cause of the complex-foods outbreaks. For each causative agent, the data from simple-food outbreaks was summarized, and the proportion of outbreaks caused by each category was used to define the probability that an outbreak i was caused by source j (Pj). For the calculation of the number of outbreaks attributed to each source, simple-food outbreaks were attributed to the single food category in question, and complex-food

outbreaks were partitioned to each implicated category relative to the probability that that outbreak could be attributed to the category as defined by Pj. As a result, outbreaks due to a complex food were only attributed to categories that had been implicated in at least one outbreak due to a simple food. As an example, outbreaks caused by chilli con carne would be attributed to the categories beef, vegetables, grains and beans, and oils and sugar. If any of these categories was not implicated in any pathogen-specific outbreak caused by simple foods, the category would be excluded from the calculations for the attribution of outbreaks to the ingredients composing the complex food. For categories implicated also in simple food outbreaks, the proportion of disease in complex food outbreaks was estimated based on the defined prior. The total number of outbreaks caused by each category in simple and complex food outbreaks was then summed, and the proportion of disease attributed to each source was estimated on the basis of the total number of outbreaks analyzed.

Table 4. Parameters used to estimate the number of reported outbreaks attributed to food sources and water.

Notation	***Description***	***Calculation***
I	Outbreak observation	-
J	Source	-
T	Year	-
sourceSj	Total number of simple-food outbreaks caused by source *j*	Sum
Totals	Total number of simple-food outbreaks, in the whole time period and in all countries	Sum
$totalnumberoutbreaks_{c;}$ $totalnumberoutbreaks_{t}$	Total number of outbreaks reported in country *c* or in time period *t*	
P_j	Probability that an outbreak *i* was caused by source *j*	Beta(sourceS*j*+1, totalS-sourceS*j*+1)
sourceSjc; sourceSjt	Total number of simple-food outbreaks caused by source *j* in country *c* or in decade *t*	Sum
sourceCjc; sourceCjt	Number of complex-food outbreaks attributed to source *j* in country *c* or decade *t*	(P[j] * F[j,i]) / sum(P [j] * F[j:J,i])
F_{ij}	Implicated food categories *j* in outbreak *i*	Data
$Total_{jc}$; $Total_{jt}$	Total number of outbreaks attributed to source *j* in country *c* or in time period *t*	*sourceSjc* or *sourceSjt* + *sourceCjc* or *sourceCjt*
$Attrib_j$	Proportion of disease attributed to source *j*	($Total_j$ *100)/$Totalnumberoutbreaks_{c/t}$

The proportion of disease attributable to specific sources was estimated only on the basis of the number of reported verified outbreaks, and the number of ill people implicated in the outbreaks was not considered in the analysis. The number of reported cases was not used in an attempt to avoid potential overestimations of the proportion of disease attributed to sources that caused large outbreaks, e.g. waterborne outbreaks.

A Markov Chain Monte Carlo simulation, specifically the Gibbs sampler, was applied to arrive to the posterior distributions for P_j. Five independent Markov chains of 40,000 iterations were run. For each chain, a different set of starting values for the priors, widely dispersed in the target distribution, was chosen. Convergence was monitored using the methods described by Gelman and Rubin (1992) and was considered to have occurred when the variance between the different chains was no larger than the variance within each individual chain, and when the chains had reached a stable level. The model was set up in WinBugs 1.4.

Different analyses took into account year of reporting of outbreaks and region. For the latter, the European regions as defined by the United Nations were used (Pires *et al.*, 2010a).

4. Results

4.1. Source attribution analysis based on microbial subtyping

The relative importance of the sources broilers, pigs, turkeys and layers, as well as the proportion of cases that was travel- or outbreak-associated were estimated at the EU level, by EU region and for countries individually.

The first part describes the overall attribution estimates at the EU level. This is followed by the results broken down on regions and countries in which the human cases were reported. The final part present attribution estimates by the country in which the food was produced (country of origin).

4.1.1. Source attribution of human salmonellosis in the EU

The most important source of human salmonellosis at the EU level was estimated to be the laying hen reservoir (i.e. eggs), with 43.8% (95% Credibility Interval (CI) 43.2 – 44.4%) of cases attributed to this source, followed by pigs (26.9%, 95% CI 26.3-27.6%). Turkeys and broilers were estimated to be less important sources of *Salmonella*, contributing with 4.0% (95% CI 3.8-4.3%) and 3.4% (95% CI 3.1-3.7%), respectively. A total of 9.2% of all salmonellosis cases were reported as being travel-related, and 3.6% of cases were reported as being part of outbreaks with unknown source. Nine percent of cases could not be attributed to any source included in the model (Table 5).

Table 5. Proportion of human reported cases attributed to food-animal sources in EU MS (median and 95% Credibility Interval (CI))

	%	95% CI	
Broilers	3.4	[3.1,	3.7]
Pigs	26.9	[26.3,	27.6]
Turkeys	4.0	[3.8,	4.3]
Layers	43.8	[43.2,	44.4]
Outbreaks[(b)]	3.6		
Travel	9.2		
Unknown	9.0	[8.7,	9.3]

(a) The proportions of outbreak- and travel-related cases were derived directly from the reported data (i.e. they were not estimated and consequently no Credibility Intervals were calculated).

(b) Includes outbreaks with unknown source. Outbreak cases for which the source was identified were assigned to the correspondent animal sources.

Within the four food-animal reservoirs the most important serovars contributing to human salmonellosis are presented in Table 6. *S.* Enteritidis infections were found to be closely associated with laying hens, whereas *S.* Typhimurium infections primarily originated from the pig reservoir. Compared to infections attributed to layers and pigs, a larger proportion of broiler- and turkey-associated cases were caused by other serovars than *S.* Enteritidis and *S.* Typhimurium, although these serovars still constituted a significant burden.

Table 6. Estimated proportion of human reported cases by food-animal source and the top-5 serovar within each source.

Broiler-associated cases		**Layer-associated cases**		**Pig- associated cases**		**Turkey-associated cases**	
Serotype	**%**	**Serotype**	**%**	**Serotype**	**%**	**Serotype**	**%**
***S.* Enteritidis**	56.9	***S.* Enteritidis**	95.9	***S.* Typhimurium**	63.1	***S.* Enteritidis**	30.4
***S.* Infantis**	10.7	***S.* Typhimurium**	1.9	***S.* Enteritidis**	28.3	***S.* Typhimurium**	28.0
***S.* Typhimurium**	8.8	***S.* Infantis**	0.8	***S.* Derby**	1.9	***S.* Newport**	8.4
***S.* Virchow**	6.9	***S.* Virchow**	0.4	***S.* Infantis**	1.5	***S.* Saintpaul**	7.0
***S.* Kentucky**	5.0	***S.* Kentucky**	0.2	***S.* Newport**	0.8	***S.* Hadar**	7.1
Others	11.7	**Others**	0.8	**Others**	4.4	**Others**	19.0
Total cases	14,334	**Total cases**	184,641	**Total cases**	113,520	**Total cases**	17,049

4.1.2. Source attribution of human salmonellosis in EU regions by reporting country

When analysing the results by EU region, layers revealed to be the most important source in Northern, Eastern and Western Europe, with between 30.0% and 59.4% of the *Salmonella* reported cases attributed to this source. This source was also important in Southern Europe (28.4% cases), but was overtaken by pigs that were estimated to contribute with 43.6% of the cases (Table 7). Overall, these sources were estimated to be the two larger contributors for disease, whereas turkeys and broilers contributed with varying but lower proportions of reported cases. A large proportion of the reported *Salmonella* infections in Northern European countries were acquired abroad, whereas foreign travel revealed to be of less importance in other regions.

Table 7. Proportion of *Salmonella* cases attributed to food sources in the EU regions[(a)], 2007-2009, median and 95% Credibility Interval (%).

	Eastern EU		Northern EU		Western EU		Southern EU	
		95% CI[(b)]		95% CI[(b)]		95% CI[(b)]		95% CI[(b)]
Broilers	7.0	[6.4 , 7.6]	1.2	[1.0 , 1.4]	2.1	[1.8 , 2.5]	3.1	[2.6 , 3.6]
Pigs	22.7	[21.5 , 23.9]	10.6	[10.0 , 11.1]	34.1	[33.5 , 34.7]	43.6	[42.5 , 44.8]
Turkey	2.2	[2.0 , 2.5]	7.4	[6.9 , 8.0]	4.1	[3.8 , 4.3]	7.6	[6.8 , 8.4]
Layers	59.4	[58.1 , 60.6]	30.0	[29.4 , 30.6]	41.8	[41.3 , 42.3]	28.4	[27.5 , 29.3]
Outbreak[(c)]	5.4		4.0		2.2		4.2	
Travel	0.8		34.5		4.8		0.7	
Unknown	2.5	[1.9 , 3.1]	12.4	[11.8, 13.0]	10.9	[10.5, 11,4]	12.5	[11.4, 13.5]

(a) EU regions as defined by the United Nations (Pires et al., 2010b). Eastern Europe: Czech Republic, Hungary, Poland and Slovakia. Northern Europe: Denmark, Estonia, Finland, Ireland, Latvia, Lithuania, Sweden and the United Kingdom. Southern Europe: Cyprus, Greece, Italy, Portugal, Slovenia, Spain. Western Europe: Austria, Belgium, France, Germany, Luxembourg and the Netherlands.

(b) The proportions of outbreak- and travel-related cases were derived directly from the reported data (i.e. they were not estimated and consequently no Credibility Intervals were calculated).

(c) Includes outbreaks with unknown source. Outbreak cases for which the source was identified were assigned to the correspondent animal sources.

4.1.3. Source attribution of human salmonellosis in 24 MSs by reporting countries

The laying hen reservoir (i.e. eggs) was estimated to be the most important source of salmonellosis in 13 countries (Austria, Czech Republic, Estonia, Germany, Greece, Hungary, Latvia, Lithuania, Luxembourg, Slovenia, Slovakia, Spain and the United Kingdom), whereas pigs were the larger contributor for salmonellosis in eight (Belgium, Cyprus, Finland, France, Ireland, Italy, Poland and Sweden); the proportion of disease attributed to layers and pigs were similar in the Netherlands. In Denmark, the most important food-animal source was estimated to be turkeys, and broilers were the major source in Portugal. It should be noted that country-specific estimates for domestically acquired cases include both domestically produced and imported food. In Finland and Sweden, the majority of *Salmonella* infections were estimated to be travel-related. Travel was also an important source, although to a lower extent, in Ireland, the UK and Denmark.

Figure 2 shows the proportions of cases attributable to each source (proportion attributed to "unknown" excluded). Tables presenting the proportion of *Salmonella* human reported cases attributed to each animal reservoir, travel and unknown sources in each country can be found in Appendix D.

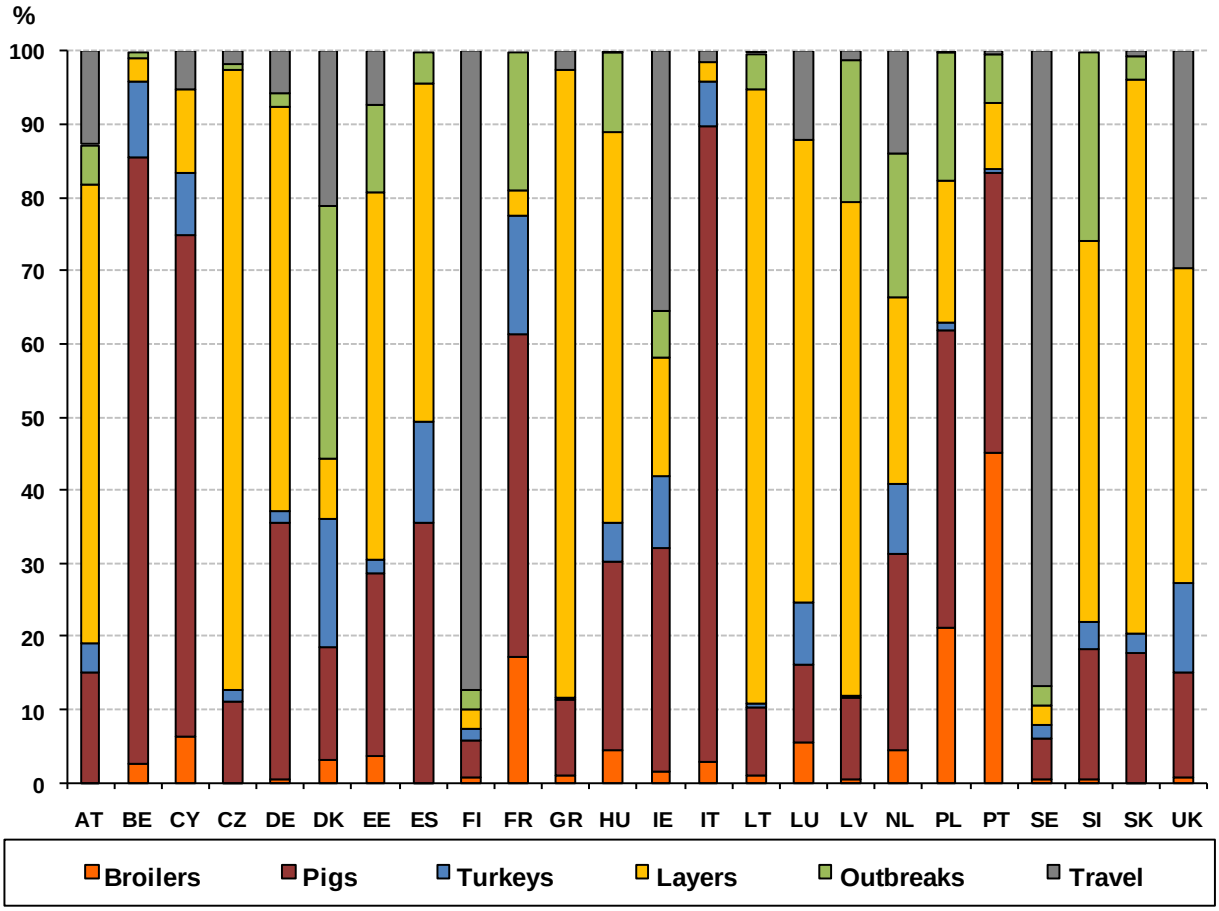

Figure 2. Proportion of *Salmonella* human cases attributed to food animal reservoirs, travel and outbreaks in 24 EU Member States, 2007-2009 (median %).

The estimated proportion of *Salmonella* cases that were attributed to the four sources in each country is presented in Table 8. A large proportion of all *Salmonella* cases occurred in Germany (34%), Czech Republic (10%) and the United Kingdom (9%). As for national totals, countries with higher proportion of cases attributable to layers included the Czech Republic (85%), Lithuania (83%) and Greece (79%), whereas the larger proportion of cases attributed to pigs were estimated to have occurred in Belgium (74%), Italy (73%) and Cyprus (51%). Although the remaining two sources were not considered to have as large an impact as layers and pigs, the largest proportion of salmonellosis attributtable to broilers was observed in Portugal (40%), and to turkeys in Denmark (15%). In Finland and Sweden, 83% and 78% of cases were related to travel, respectively. The proportion of cases that could not be attributed to any of the sources included in the model varied from 0.6% in Latvia to 32% in France. This proportion was lower than 15% in 19 out of 24 MSs. Member State-specific estimates with 95% Credibility Intervals and showing

proportions before assigning outbreak-related cases with an identified source to one of the four food-animal reservoirs can be found in Appendix D.

Table 8. Proportion (%) of *Salmonella* cases attributable to animal sources, travel and outbreaks in EU MSs, 2007 to 2009.

	Broilers	Pigs	Turkeys	Layers	Outbreaks[(a)]	Travel	Unknown	Total
AT	0.3	13.8	3.6	58.5	3.2	11.6	9.0	8,460
BE	2.3	74.0	9.2	2.9	0.5	0.0	11.2	10,917
CY	4.8	51.3	6.3	8.7	0.0	3.8	25.1	461
CZ	0.1	10.9	1.7	84.6	0.2	1.7	0.8	39,032
DE	0.5	32.7	1.3	51.2	1.6	5.2	7.5	129,704
DK	2.8	15.6	15.1	10.5	23.8	18.2	14.1	7,461
EE	10.6	24.4	1.8	49.0	4.7	7.1	2.3	1,338
ES	0.1	31.8	12.4	41.5	3.9	0.0	10.3	12,419
FI	0.6	4.9	1.7	2.5	2.3	83.2	4.8	8,228
FR	12.8	32.5	11.1	6.9	4.8	0.0	32.0	19,849
GR	0.8	9.5	0.3	78.6	0.0	2.3	8.3	2,154
HU	4.2	24.3	4.9	49.7	9.5	0.2	7.3	19,244
IE	1.4	26.0	8.4	14.2	5.0	30.3	14.7	1,223
IT	2.3	73.2	5.3	2.1	0.0	1.3	15.8	11,887
LT	1.6	9.1	0.7	82.8	4.4	0.3	1.2	7,641
LU	4.3	8.4	6.8	50.0	0.0	9.6	20.9	527
LV	3.5	12.2	0.2	69.2	13.2	1.2	0.6	2,664
NL	3.9	22.9	8.1	27.2	11.3	11.9	14.7	4,077
PL	21.8	39.8	1.0	23.8	11.3	0.1	2.2	29,268
PT	40.2	34.2	0.5	8.1	6.0	0.3	10.7	1,036
SE	0.5	4.9	1.7	2.4	2.3	77.7	10.5	11,169
SI	0.3	16.0	3.1	47.3	21.9	0.0	11.4	2,995
SK	0.1	17.5	2.5	75.2	2.3	0.8	1.7	15,879
UK	0.6	11.7	10.1	35.5	0.0	24.3	17.8	35,972

(a) Outbreaks with unknown source. Outbreak cases for which the source was identified were assigned to the correspondent animal sources.

The proportion of *Salmonella* reported cases attributed to each source by the country from which the food source originated (regardless of the country where the case was reported) was estimated on the basis of the amount of food source domestically produced and imported by each country. Estimates were found to be too dependent on the validity of the trade data, and thus are not presented in detail. Overall, results showed that a large proportion of broilers that resulted in *Salmonella* reported cases in the EU were produced in a single country, thus being responsible for

56% of the broiler-related cases. Similarly, 39% of the reported salmonellosis cases attributed to pigs was estimated to originate from another MS. Turkey and layer-related cases were more widely distributed with the majority of the infections originating from 8-10 countries.

4.1.4. Posterior estimates for $\mathbf{a_{cj}}$ *and* $\mathbf{q_i}$

The estimated ability of food sources to act as a vehicle for disease (a_{cj}) was higher for layers in 11 countries (Austria, Czech Republic, Estonia, Germany, Greece, Hungary, Lithuania, Luxembourg, Latvia, Slovenia and Slovakia) and turkeys in 10 countries (Belgium, Cyprus, Denmark, Finland, France, Ireland, the Netherlands, Spain, Sweden and the UK). In Italy and Poland, the highest a_{cj} was estimated for pigs, whereas in Portugal results revealed a higher estimate for broilers. Values estimated for a_{kj} are shown in Appendix E1.

Regarding the ability of different serovars to cause disease, the highest q_i value was estimated for *S.* Kentucky, followed by *S.* Enteritidis (value fixed to 1), *S.* Newport, *S.* Virchow and *S.* Typhimurium,. Estimated values for q_i for all serovars are shown in Appendix E2.

4.1.5. Goodness of fit

Results of the goodness of fit test showed that the model fit was satisfactory for the vast majority of the countries (Figure 3). Poor fit was observed for countries with poor data availability or quality, e.g. Cyprus and Luxembourg.

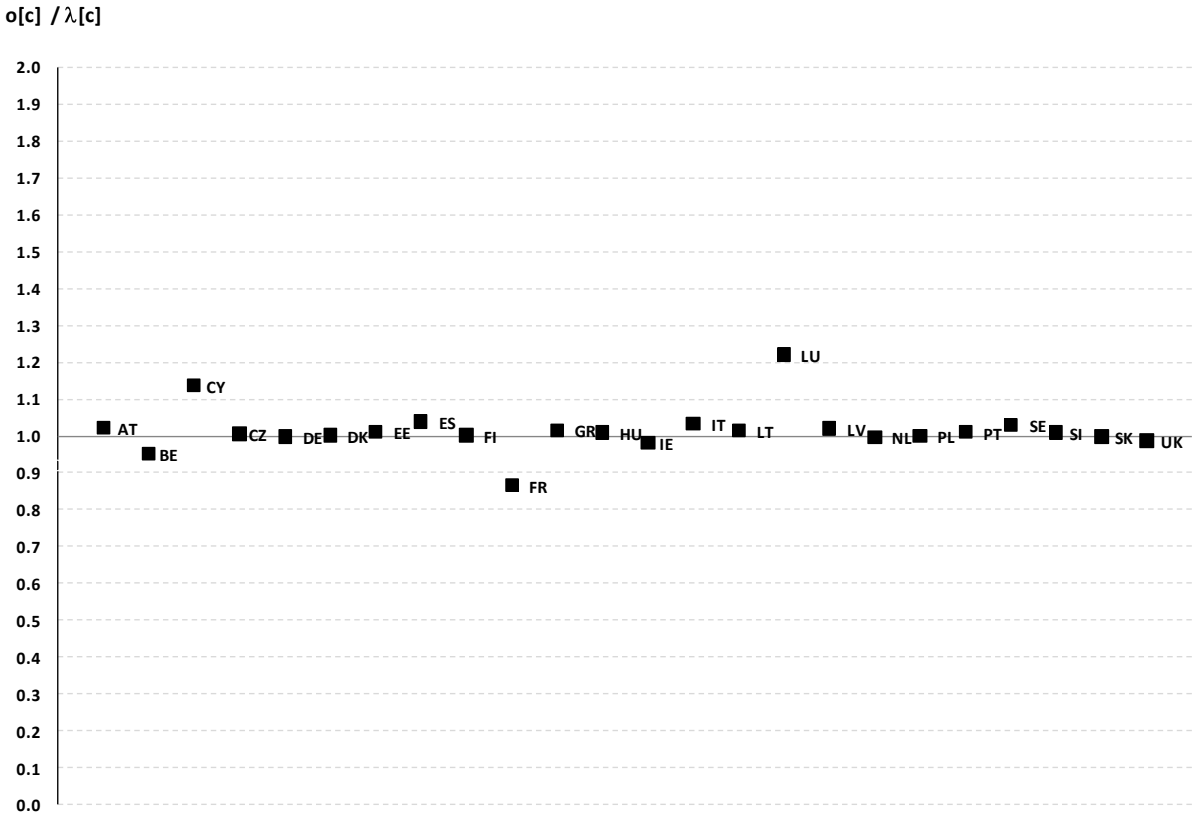

Figure 3: Ratio between observed and predicted cases of *Salmonella* in 24 EU Members States. A ratio of 1 represents a perfect model fit.

4.2. Source attribution analysis based on data from foodborne outbreaks investigations

4.2.1. Source attribution of salmonellosis in the EU

The proportion of *Salmonella* outbreaks attributed to each source in Europe varied in the studied period (Figure 4). In all years, eggs were estimated to be the most important source of disease, and pork, chicken, the general category meat and poultry, and dairy followed in importance. The relative contribution of eggs for *Salmonella* outbreaks increased from 2007 (56.1%) to 2008 (61.6%), but a substantial decrease was observed in the following year, when the proportion of outbreaks attributed to this source was estimated to be 34.5% (Table 9). Pork was estimated to be the second most important source of salmonellosis in 2007 (5.4%) and 2008 (6.1%), whereas poultry meat (10.9%) was the second contributor for disease in 2009. Chicken was estimated to

be an important source in all years, contributing to between 2.3% and 3.5% of salmonellosis in EU countries. The relative importance of pork increased slightly from 2007 to 2008, but results showed a decrease in 2009 (1.8%). Dairy products, seafood and vegetables were also estimated to be sources of salmonellosis. The proportion of outbreaks that could not be attributed to any source varied substantially over the years and was higher in 2009 (43.5%).

Table 9. Proportion of *Salmonella* outbreaks attributed to food sources in the EU, 2007-2009, by year, median and 95% Credibility Interval (%).

	2007		**2008**		**2009**	
Eggs	56.1	[56.0,56.3]	61.6	[61.4,61.7]	34.5	[34.3,34.6]
Dairy	2.2	[2.1,2.3]	2.9	[2.7,3.0]	1.2	[1.1,1.3]
GoatMilk	0	[0,0]	0	[0,0]	0	[0,0]
Meat	1.1	[1.1,1.12]	3.3	[3.3,3.4]	1.3	[1.3,1.4]
Poultry	0	[0,0]	0.2	[0.2,0.2]	10.9	[10.9,10.9]
Chicken	3.5	[3.5,3.5]	2.3	[2.2,2.3]	2.6	[2.5,2.6]
Ducks	0	[0,0]	0	[0,0]	0	[0,0]
Turkey	0.5	[0.5,0.5]	0.04	[0.03,0.06]	0.3	[0.3,0.3]
Beef	0.5	[0.5,0.6]	0.6	[0.5,0.7]	0.6	[0.6,0.6]
Pork	5.4	[5.4,5.4]	6.1	[6.1,6.1]	1.8	[1.8,1.8]
Lamb	0.2	[0.2,0.2]	0		0	
Mutton	0		0		0	
Game	0		0		0	
FruitsNuts	0.2	[0.2,0.2]	0.2	[0.2,0.2]	0.01	[0.005,0.03]
Vegetables	2.4	[2.3,2.4]	1.0	[0.8,1.1]	1.5	[1.4,1.6]
GrainsBeans	0.8	[0.7,0.9]	0.7	[0.5,0.8]	0.4	[0.3,0.4]
OilsSugar	0.9	[0.8,1.0]	0.2	[0.1,0.3]	0.8	[0.7,0.8]
Seafood	0.8	[0.8,0.8]	2.4	[2.4,2.5]	0.9	[0.8,0.9]
Water	0.5	[0.5,0.5]	0		0	
Unknown	25.0		18.5		43.5	

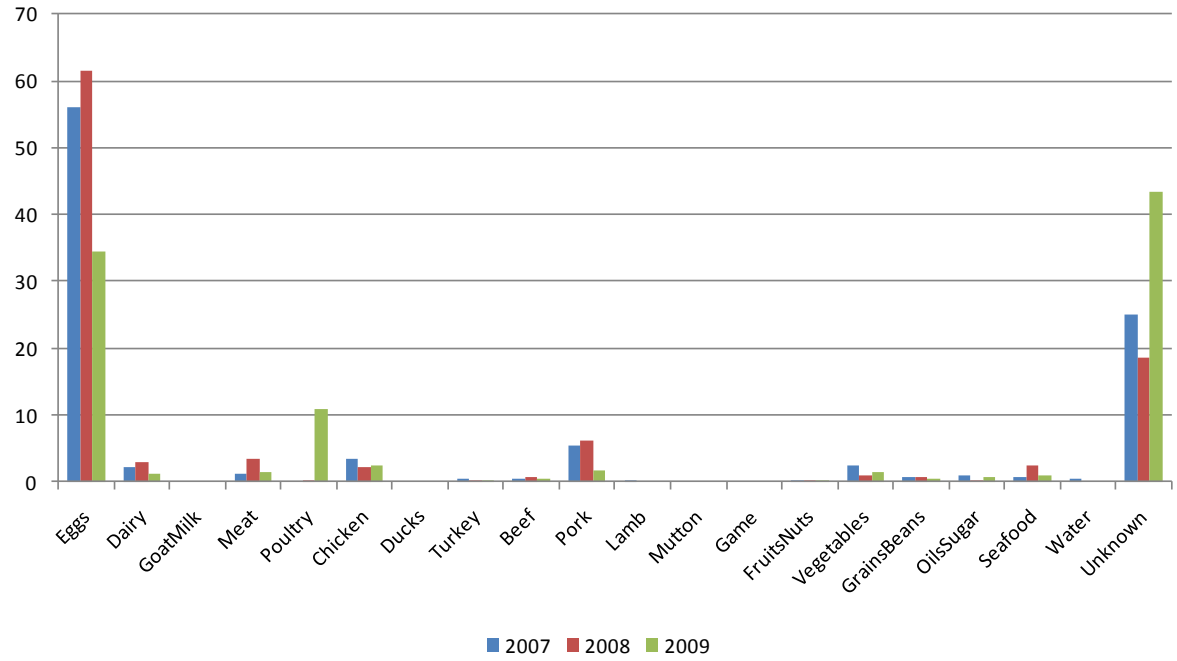

Figure 4: Proportion of *Salmonella* outbreaks attributed to food sources in 29 EU countries, 2007-2009 (median %).

4.2.2. Source attribution of salmonellosis by EU regions

The source attribution analysis by region was performed encompassing data from the whole study period (2007 to 2009). Results showed a substantial variability in the importance of sources between regions and in the proportion of outbreaks attributed to an unknown source (Figure 5; Table 10). Eggs were estimated to be the most important source of salmonellosis in all regions, source attribution estimates being higher in Eastern Europe (76.2%) and Southern Europe (59.9%). Pork followed in importance in Western Europe (9.5%), whereas vegetables were estimated to be a major contributor for salmonellosis in Northern Europe (9.1%). Chicken and dairy products revealed to be of importance in all regions. The proportion of *Salmonella* outbreaks attributed to an unknown source varied substantially between regions, being highest in Northern Europe (50.8%) and was lowest in Eastern Europe (9.6%).

Table 10. Proportion of *Salmonella* outbreaks attributed to food sources in the EU, 2007-2009, by region, median and 95% Credibility Interval (%).

	Eastern EU		Northern EU		Southern EU		Western EU	
Eggs	76.18	[75.85,76.47]	19.7	[19.62,19.78]	59.86	[59.81,59.91]	35.6	[35.53,35.66]
Dairy	2.4	[2.16,2.67]	3.46	[3.25,3.66]	1.15	[1.14,1.15]	2.27	[2.19,2.34]
GoatMilk	0	[0,0]	0	[0,0]	0	[0,0]	0	[0,0]
Meat	1.55	[1.54,1.57]	1.49	[1.49,1.49]	1.66	[1.66,1.66]	2.47	[2.44,2.5]
Poultry	0	[0,0]	0	[0,0]	11.08	[11.08,11.08]	0.19	[0.19,0.19]
Chicken	3.65	[3.59,3.72]	5.78	[5.74,5.83]	1.66	[1.66,1.66]	2.28	[2.27,2.3]
Ducks	0	[0,0]	0	[0,0]	0	[0,0]	0	[0,0]
Turkey	0.27	[0.26,0.29]	0.75	[0.75,0.75]	0	[0,0]	0.39	[0.39,0.39]
Beef	0.63	[0.57,0.7]	0.1	[0.06,0.16]	0.28	[0.28,0.28]	0.84	[0.82,0.87]
Pork	2.18	[2.17,2.2]	6.92	[6.84,6.99]	0	[0,0]	9.54	[9.51,9.58]
Lamb	0.02	[0.007,0.04]	0	[0,0]	0	[0,0]	0.19	[0.19,0.19]
Mutton	0	[0,0]	0	[0,0]	0	[0,0]	0	[0,0]
Game	0	[0,0]	0	[0,0]	0	[0,0]	0	[0,0]
FruitsNuts	0.002	[0.0007,0.004]	0.75	[0.75,0.75]	0	[0,0]	0.25	[0.21,0.29]
Vegetables	0.47	[0.41,0.52]	9.1	[8.93,9.3]	1.08	[1.04,1.14]	1.19	[1.08,1.3]
GrainsBeans	1.21	[1.04,1.42]	0.49	[0.32,0.68]	0.35	[0.32,0.39]	0.41	[0.34,0.5]
OilsSugar	1.53	[1.4,1.7]	0.13	[0.09,0.18]	0.1	[0.07,0.14]	0.38	[0.32,0.45]
Seafood	0.25	[0.25,0.26]	0.58	[0.51,0.63]	3.11	[3.05,3.16]	1.28	[1.26,1.29]
Water	0	[0,0]	0	[0,0]	0.83	[0.83,0.83]	0	[0,0]
Unknown	9.63		50.75		18.84		42.72	

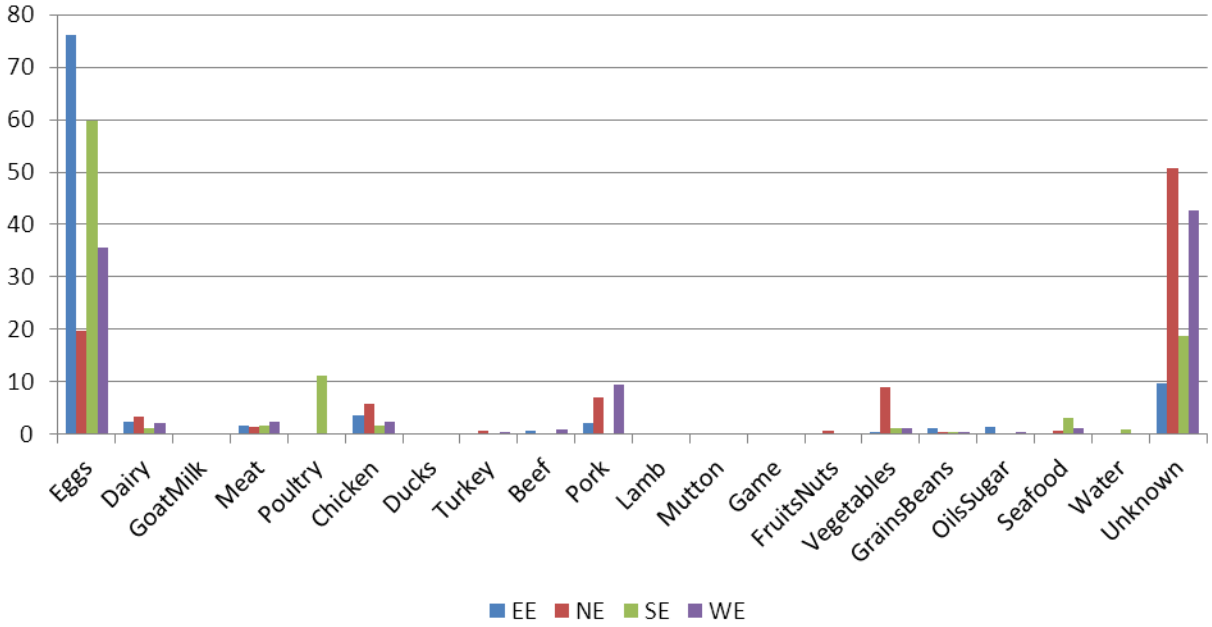

Figure 5: Proportion of *Salmonella* outbreaks attributed to food sources by EU region, 2007-2009 (median %).

5. Discussion

Identification of the most important sources of foodborne illness is essential to prioritize and define effective food safety interventions aimed at reducing the public health burden of disease. *Salmonella* is one of the most important foodborne pathogens in the EU, and source attribution of human salmonellosis has been conducted in a number of European countries. However, all studies were conducted in countries with well-established monitoring programmes and effective public health and animal production surveillance systems (Hald *et al*., 2004; Whalström *et al*., in press; Valkenburgh *et al.*, 2007). The relative contribution of different food sources is expected to vary between countries, influenced by food production systems, food consumption and preparation habits, food trade and the epidemiology of the pathogen in different regions. *Salmonella* source attribution in the majority of EU Member States has thus far not been conducted.

Reflecting the efficiency of public health and food-animal surveillance systems, the availability of data for *Salmonella* source attribution studies varied substantially among EU MSs. In this report, available data from EU MSs was compiled to attribute human salmonellosis to food-animal sources in each country and to derive estimates for the relative importance of sources of *Salmonella* in the EU and EU regions.

To estimate the relative contribution of food-animal sources for salmonellosis in the EU, two source attribution methods were used: a microbial subtyping approach and an analysis of data from outbreak investigations. Different sets of data were used for each model, but both covering the same time period (2007 to 2009). For the microbial subtyping approach, reported human sporadic cases and EU monitoring or Baseline Survey data from food-animal sources from 24 countries were applied. For the analysis of outbreak data, information consisted of the number of *Salmonella* outbreaks that have been investigated in 29 countries and reported to EFSA, with information of the implicated food source for solved outbreaks. The difference in the number of countries included in the two models reflects the data availability. The food sources also differed: four food-animal reservoirs were included in the microbial subtyping model and 19 in the outbreak model, including water. The latter reflects a food classification scheme that is described hierarchically and where some main categories may include several food sources, depending on the level of detail of the available data. The sources included in the two models represent distinct levels of the food production chain: in the microbial subtyping model, sources represent the origin of the food at the animal production level (e.g. *layers* instead of *eggs; pigs* instead of *pork*), whereas in the model using outbreak data the sources represent the foods at the end of the production chain i.e. at the point of consumption. Still, the relative importance of sources as estimated by the two methods is comparable, and for example the proportion of salmonellosis attributed to layers in one method can be faced with the attribution estimate for eggs in the other.

Results of the microbial subtyping approach suggest that layers were the most important source of salmonellosis, being responsible for nearly 50% of *Salmonella* infections in the EU in general and being the larger contributor for disease in three EU regions. Layers were estimated to be the most

important source of salmonellosis in Austria, Czech Republic, Estonia, Germany, Greece, Hungary, Latvia, Lithuania, Luxembourg, Slovenia, Slovakia, Spain and the United Kingdom. Pigs was estimated to be the second largest contributor for salmonellosis in the EU, and results showed this was the most important source of *Salmonella* in eight countries: Belgium, Cyprus, Finland, France, Ireland, Italy, Poland and Sweden. In the Netherlands, similar proportions of disease were attributed to these two sources. Turkeys revealed as particularly important only in Denmark, whereas broilers were the major source in Portugal.

The proportion of *Salmonella* cases attributed to each source by the country from which the food source originated was also estimated. These estimates took into account the amount of food produced and traded between countries as reported to the EUROSTAT database and the underlying assumption was that these data reflected the real flow of foodstuffs and thus exposure in the countries. Results suggested variability in the relative contribution of food-animals produced in different countries depending on imports, but were found to be too dependent on the validity of the trade data to be presented in detail. Estimates should be interpreted with care.

No distinction was made between travelling within or outside Europe since this information was often lacking. A large proportion of cases reported in Finland, Sweden, Ireland, the UK and Denmark were attributed to international travel. Travel was less important in remaining countries, varying from 14% in the Netherlands to 0% in e.g. Spain. The estimated high proportion of cases acquired abroad in Sweden is supported by a previous source attribution study, where 82% of *Salmonella* infections were attributed to travel (Wahlström *et al.*, in press). In Denmark, previous studies suggest that the proportion of travel-related *Salmonella* cases varied between 22 and 46% in the period from 2007 to 2009 (Anon., 2010), but these have been calculated accounting for the probability of a case with unknown travel information having been travelling abroad before onset of symptoms, and thus add more "possible" travellers. In this model, the proportion of travel-related cases was calculated on the basis of the cases that were reported as acquired outside the country, which is dependent on the patients being asked whether they have been travelling abroad before onset of symptoms, and the information being registered centrally. Travel information is considered to be underreported in most EU MSs, which may explain the difference in the proportion of cases attributed to travel in EU countries. Because all reported cases with missing travel information were assumed to be domestically acquired, travel-related disease is in general expected to be underestimated.

The variability observed in the number of reported human *Salmonella* infections reflects true differences in the burden of salmonellosis in different countries, but also of differences in foodborne disease surveillance systems in MSs, where the proportions of *Salmonella* cases occurring in the population that are diagnosed, of the samples that are collected from diagnosed patients, and of the laboratory-confirmed cases that are reported differ, and where different typing protocols are applied. The loss of data at various points along the surveillance chain from patient to official statistics is recognized in all countries (Wheeler et al., 1999) and results in different degrees of underreporting. One way to deal with underreporting is the application of country-specific multiplying factors based on Swedish travellers' data (de Jong and Ekdahl, 2006; EFSA,

2011b). Because the rate of underreporting varies substantially between countries, the burden of salmonellosis is expected to differ greatly when compared to the estimates derived from "raw" reported surveillance data. The expected differences should, therefore, be considered when comparing the contribution from each country to the total burden of human salmonellosis in the EU.

Availability of animal data varied between countries. Not all countries included in the microbial subtyping model participated in the EFSA BSs, which resulted in the absence of data for some countries. To fill these data gaps, the most recent data from the EFSA CSR were used. Because no BS has been conducted in cattle and there is at this point no EU harmonized monitoring in place, data from the cattle reservoir were not included in the model. The consequence of this may be that a proportion of human cases were wrongly attributed to a reservoir with a similar serovar distribution, e.g. pigs. Still, national attribution studies have suggested that the contribution from the cattle reservoir in general is lower than for pigs (Pires *et al*, 2008; Pires and Hald, 2010).

Other foods recognized as sources of human salmonellosis such as fruit and vegetables were also not included. However, it is emphasised that the subtyping approach employed is tracing human infections back to the animal reservoir of origin. This means that human infections caused by fruits and vegetables contaminated with faeces from an animal reservoir would be traced back to this reservoir, which for some type of risk management decisions may be appropriate. Still, there is evidence that *Salmonella* contaminated foodstuffs are imported into EU from third countries. Such foodstuffs obviously constitute a risk for humans, but their relative importance could not be accounted for in the model. From the results of the attribution study using outbreak data, foodstuffs like vegetables appeared to be most important in Northern Europe.

Another data limitation for the subtyping approach was linked to reporting of aggregated data or data with no or sparse serotyping information by some countries. To overcome this, records were reassigned based on defined criteria. Additionally, whenever possible countries were approached directly for more complete data sets. These issues as well as the lack of further subtyping information (e.g. phage typing) on *S.* Enteritidis and *S.* Typhimurium may have resulted in attribution of some human cases to the wrong source. For instance, phage typing of *S.* Enteritidis would most likely have resulted in a better distinction between the broiler and the laying hen reservoir in MSs, where *S.* Enteritidis is widely prevalent in both sources.

To assess the relation between the observed *Salmonella* cases (sporadic human cases reported in each country) and the number of cases predicted by the microbial subtyping model and attributable to sources in each country, a ratio between these two parameters was estimated. Estimates for the majority of the countries were very close to 1, suggesting that predictions of the model matched the surveillance reports. Exceptions included Belgium and France, for which the number of expected cases attributable to sources was higher than observed cases, and Cyprus and Luxembourg, where the model underestimated the number of *Salmonella* cases attributable to sources. These estimates reflect the quality and amount of data available for the model, which varied substantially between countries and which influenced the model results in general.

In the source attribution model using outbreak data, data from verified outbreak investigations were analysed 1) by year so that trends and changes in the relative importance of sources of *Salmonella* in the study period could be assessed, and 2) by region, merging the three years of data together, in order to compare the relative contribution of food sources between EU regions. Due to the limited number of outbreaks reported by individual countries, analyses by country were not possible. Results suggest that eggs were the most important source of salmonellosis in Europe in the period between 2007 and 2009. The relative contribution of this source for disease varied over the years and between regions, being particularly important in Eastern and Southern and Europe, but having decreased in 2009 in the EU in general. The estimated regional differences are supported by the variability in the prevalence of *Salmonella* Enteritidis in layer hens in EU Member States (EFSA, 2007d) and are in line with previous source attribution estimates (Pires et al., 2010b), but suggest an increase in the proportion of salmonellosis attributable to eggs in Southern Europe. The decrease in the relative importance of this source in the EU in 2009 may be associated with the recently imposed EU standards for the prevalence of *S*. Enteritidis in laying hens and consequent implemented control strategies in several Member States.

The contribution of other food sources for salmonellosis was substantially lower in all regions during the whole time period. Pork was the second most important source in Western and Northern Europe, whereas poultry in Southern Europe and chicken in Eastern Europe followed eggs in the attribution estimate. The estimated decrease in the relative contribution of the source category meat for salmonellosis may be linked to a more detailed specification of the implicated source of the outbreak by the individual countries when reporting. The increase in the proportion of disease attributable to poultry in 2009 supports this hypothesis. The proportion of outbreaks attributed to an unknown source was high in all years and increased in 2009. The source attribution analysis by region showed that the proportion of unsolved outbreaks was higher in Northern Europe and relatively low in remaining regions. This difference is expected to be a consequence of a less efficient surveillance of foodborne outbreaks in several countries, which results in the investigation of fewer outbreaks and in the reporting of solved outbreaks only.

The frequency of reporting of outbreak related cases also varied between countries and over the three year period, as did the proportion of outbreaks that were investigated and for which a causative food source was identified. These data inconsistencies influenced source attribution estimates and hampered regional comparisons of the most important sources of disease. Data from verified outbreaks was chosen over the total number of reported outbreaks to ensure that only confirmed outbreaks were used to inform the source attribution estimates. However, substantial differences in the number of reported outbreaks in different countries have been reported, which is reflected in the amount of data available in these countries and consequently on the influence of these countries in the final estimates. For example, France, Poland and Spain together reported over 80% of verified outbreaks in the study period, which is likely to have driven the results to reflect these countries epidemiology of *Salmonella* as opposed to the variety of EU MSs.

The estimated relative importance of food-animal sources for salmonellosis in the EU estimated by the two source attribution approaches was in agreement, although not comparable in absolute numbers. Results from both models suggested that layers/eggs were the most important source of salmonellosis in the EU, and that pigs/pork followed in importance in most EU regions. The proportion of disease attributed to pork in the outbreak model was substantially lower than the estimate obtained in the microbial subtyping model, which is likely to be a consequence of the distinct points of attribution of the methods: pork and pork products are traditionally consumed well cooked, and thus the risk of salmonellosis after consumption of a contaminated product decreases after heat-processing. Still, contaminated pork products may cross-contaminate other sources (food or environmental routes) and consequently result in human disease. In general, the microbial subtyping approach attributes human illness at the reservoir level, i.e. at the origin of the pathogen, and does not account for the transmission route from the source until human exposure. Consequently, disease attributed e.g. to the reservoir *pigs* may be due to consumption of pork or pork products, to direct or indirect contact with pigs, or to environmental contamination originating from pig farms. In contrast, source attribution by an analysis of outbreak data attributes disease to the point of exposure, i.e. to the food item that was consumed, regardless of the step in the food production chain where this food was contaminated. As a result, a *Salmonella* outbreak may be attributed to e.g. vegetables, even if disease was caused by salad that was cross-contaminated from an animal product during meal preparation. Thus, a method that focuses on the point of reservoir is expected to attribute a higher proportion of disease to this source (in this case, *pigs*) than a method that attributes at the point of exposure (*pork*). This emphasises that the two methods are useful to address different public health questions and results should be seen accordingly.

In addition to attributing human illness at different points of the farm-to-consumption continuum, the two approaches require the availability of different data, and utilize different statistical methods. Thus, comparisons of results should be made with care. Additionally, even though the same time period was used in the two analyses, included countries varied and human salmonellosis was attributed to a different number of sources. Limitations of the use of outbreak data for attribution have been discussed (Pires *et al.*, 2009): firstly, outbreaks may not be representative of all human cases occurring in the population, and source attribution of outbreak-related and of sporadic disease is expected to give different signals; additionally, certain food vehicles are more likely to be associated with reported outbreaks than others, which can lead to an overestimation of the proportion of human illness attributed to a specific food.

Despite data limitations and the resulting uncertainty in the results, the source attribution estimates are considered valid as a first indication of which sources are most important for human salmonellosis in several countries, and highlight regional differences in the contribution of different food-animal sources for disease and on the efficiency of surveillance systems in place in EU Member States. The results are expected to be useful for the delineation of risk management strategies. Although, the overall conclusions reached by the two source attribution approaches agree, the more detailed results differ. This may be used to inform risk managements interventions at different points of the food production chain.

CONCLUSIONS AND RECOMMENDATIONS

CONCLUSIONS

- The reported number of *S.* Enteritidis cases in EU has been decreasing from 2007 to 2009. The improved surveillance and control of *S.* Enteritidis in laying hens in many MSs is assessed to be responsible for at least part of this reduction.
- In contrast, the number of *S.* Typhimurium infections has increased (although with a small decline from 2008 to 2009) indicating that one or more sources of these infections are increasing in importance.
- Results of the microbial subtyping approach indicated that the laying hen reservoir (i.e. eggs) was the most important source of human salmonellosis, being responsible for 48.1% (95% CI: 47.5-48.8%) of *Salmonella* infections in the EU in general and being the larger contributor for disease in three EU regions and in 13 EU MSs. This was supported by the source attribution analysis based on outbreak data, where table eggs also were found to be the most important source.
- Despite the decreasing trend of human *S.* Enteritidis infections, eggs from laying hens are still considered to be the single most important source of *S.* Enteritidis infections in EU.
- The pig reservoir was estimated to be the second largest contributor to human salmonellosis in the EU responsible for 29.6% (95% CI: 28.9-30.3%) of the reported cases, and the results showed that it was the most important source in eight countries.
- The results further indicated that the pig reservoir was responsible for the majority of the human *S.* Typhimurium infections.
- Turkeys and broilers were estimated to contribute with 4.4% (95% CI 4.2-4.7%) and 3.7% (95% CI 3.4-4.0%) of all human salmonellosis cases. A relatively large proportion of cases (app. 35-40%) originating from these reservoirs were estimated to be caused by other serovars than *S.* Enteritidis and *S.* Typhimurium.
- The relative importance of different food-animal sources was found to vary across EU regions and between countries according to differences in prevalences, trade and consumption patterns and preferences, and animal and food production systems.
- The laying hen reservoir revealed to be the most important source in Northern, Eastern and Western Europe, with between 30.0% and 59.4% of the *Salmonella* reported cases attributed to this source, whereas pigs were the major source of salmonellosis in Southern Europe, contributing with 43.6% of the cases. A large proportion of the reported *Salmonella* infections in Northern European countries were acquired abroad.
- Some *Salmonella* reservoirs (e.g. cattle/beef) were not included in the model due to poor data availability and quality. It is therefore likely that the contribution of the human

salmonellosis cases allocated to the animal reservoirs included in the model, particularly pigs, have been overestimated.

- Besides the statistical uncertainty reflected in the credibility intervals in the model results, other factors contributed to the uncertainty of the validity of the results. These include the variability in the human surveillance systems in place in the countries as well as the different details with which serovar information is reported in both the human and animal food source data. Such uncertainties cannot be statistically quantified, but should be kept in mind when interpreting the results.
- The analysis of outbreak data showed that in all included years, eggs were estimated to be the most important source of disease, followed in order of importance by pork, chicken, the general category "meat and poultry", and dairy products. These results were in good alignment with results of the microbial sutyping approach even though the two approaches have different data requirements and attribute cases at different points in the farm to consumption continuum.
- Despite data limitations and resulting uncertainty in the results, the obtained source attribution estimates are considered useful for the delineation of risk management strategies. These represent the first indication of which sources are more important for human salmonellosis in several countries, and highlight regional differences in the contribution of different food-animal sources for disease and on the efficiency of surveillance systems in place in EU Member States.

RECOMMENDATIONS

- Some of the uncertainty in the results presented in this report occurred as a consequence of the lack of harmonized *Salmonella* subtyping in EU countries. It is recommended to provide more comparable subtyping data (particularly serovar, but e.g. also molecular typing and antimicrobial resistance testing) from both human and animal-food sources from all MSs. This would improve future source attribution studies and trend analysis.
- The systems for reporting of human salmonellosis cases vary considerably between MSs making it very difficult to compare incidences and the effect of EU-wide *Salmonella* control. A continuous effort to provide comparable and harmonized data on human salmonellosis in all MSs is therefore recommended. This should include efforts to quantify the level of underreporting.
- The cattle reservoir is recognized as a source of human salmonellosis, but was not included in the subtyping approach due to poor data quality. It may be considered to conduct an EU-wide baseline survey of *Salmonella* in cattle or beef to investigate the role of beef as a source of human infections.

- The microbial subtyping approach should be repeated on a regular basis (e.g. every 3 to 5 years) in order to evaluate the effect of *Salmonella* control in the various food-animal sources and to follow the trends and dynamic changes in the sources of human salmonellosis.
- The approach based on the analysis of the foodborne outbreak data should be updated annually considering several years of data in order to follow the trends in sources of human salmonellosis outbreaks, which also give useful informations of the most important sources for sporadic cases.

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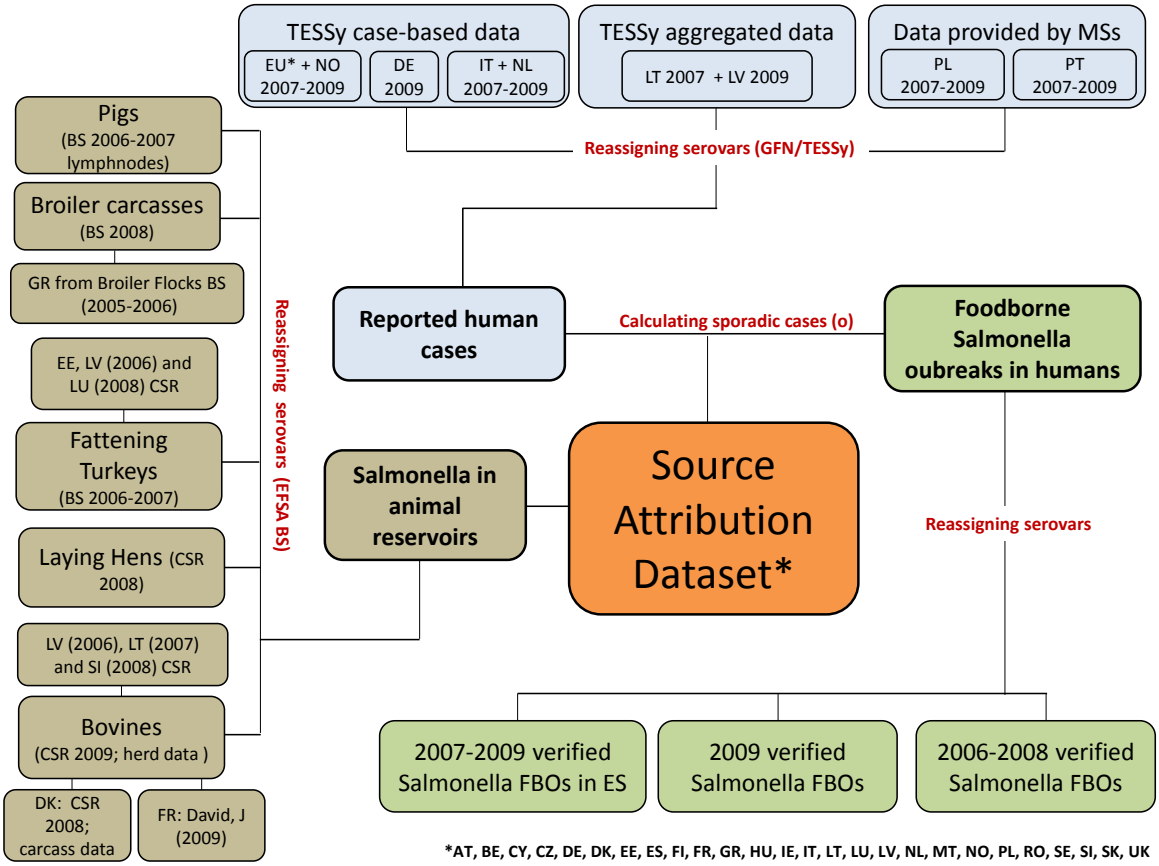
APPENDICES

APPENDIX A. AVAILABILITY OF DATA FROM THE DIFFERENT DATASETS BY COUNTRY[(a)]

Animal source	Data source	Countries	Additional data sources
Laying hens	CSR data 2008	AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GR, HU, IE, IT, LT, LU, LV, NL, NO, PL, PT, RO, SE, SI, SK, UK	
Cattle	CSR data 2007-2009	AT, BE, BG, CH, CZ, DE, DK, EE, ES, FI, FR, GR, HU, IE, IT, LT, LU, LV, NL, NO, PL, PT, RO, SE, SI, SK, UK	FR: David, J (2009); LV: CSR 2006
Pigs	BS 2006, lymph node	AT, BE, BG, CY, CZ, DE, DK, EE, ES, FI, FR, GR, HU, IE, IT, LT, LU, LV, NL, NO, PL, PT, SE, SI, SK, UK	
Broiler	BS 2008, carcasses	AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GR, HU, IE, IT, LT, LU, LV, MT, NL, NO, PL, PT, RO, SE, SI, SK, UK	GR: BS 2005/6
Turkey	BS 2006, Fattening turkeys	AT, BE, BG, CY, CZ, DE, DK, EE, ES, FI, FR, GR, HU, IE, IT, LT, LU, LV, NL, NO, PL, PT, SE, SI, SK, UK	EE: CSR 2006; LU: CSR 2008 LV: CSR 2006;
Human cases	Foodborne outbreak data, 2007-2009	AT, BE, CH, CZ, DE, DK, EE, ES, FI, FR, HU, IE, LT, LV, NL, NO, PL, PT, RO, SE, SI, SK	
	TESSy case-based and aggregated data, 2007-2009[(b)]	AT, BE, BG, CY, CZ, DE, DK, EE, ES, FI, FR, GR, HU, IE, IT, LT, LU, LV, MT, NL, NO, PL, PT, RO, SE, SI, SK, UK	
	National monitoring and laboratory surveillance data 2007-2009[(c)]	PL, PT, NL, IT, DE	

(a) If data were missing from a specific source in a country, used surrogate data sources are indicated.
(b) Bulgaria reported human cases, but no serovar information was available.
(c) Obtained through direct contact with Member States.

APPENDIX B. DIAGRAM ILLUSTRATING THE CONSTRUCTION OF THE DATASET FOR SOURCE ATTRIBUTION BASED ON MICROBIAL SUBTYPING [(a)].



(a) GFN Country Databank used as reference for serovar distributions, not as a data source.

APPENDIX C. DESCRIPTION OF DATA AVAILABLE FOR *SALMONELLA* SOURCE ATTRIBUTION BY MICROBIAL SUBTYPING

Data from 29 countries was available in different combinations of animal and human data sources. A summary of availability of information in each data source per country is presented in Appendix A. The number of countries in which each of the selected serovars was present in each data source and the number of serovars observed in each country per data source are presented in Tables C1 and C2, respectively.

Table C1. Number of countries in which each serovar is present by data source.

Serovar	Number of countries [a]							Total sources (n=7)
	TESSy	FBO[b]	Broilers	Pork	Turkey	Layers	Cattle[c]	
S. Enteritidis	27	19	15	18	17	20	25	7
S. Typhimurium	27	16	12	23	12	16	25	7
S. Virchow	26	3	7	5	2	11	1	7
S. Infantis	26	3	15	16	4	13	8	7
S. Newport	26	4	3	7	9	7	2	7
S. Derby	25	1	3	19	11	5	10	7
S. Agona	24	2	10	12	8	9	5	7
S. Hadar	24	2	10	3	10	7	3	7
S. Bredeney	24	2	8	9	6	5	2	7
S. Kentucky	22	0	6	0	1	2	0	4
S. Braenderup	23	0	2	3	2	7	1	6
S. Saintpaul	22	1	2	2	11	4	1	7
S. Brandenburg	23	1	1	7	0	4	2	6
S. Montevideo	22	0	8	9	3	10	4	6
S. London	22	0	1	8	1	1	2	6
S. Bovismorbificans	22	4	0	7	0	1	2	5
S. Stanley[c]	21	1	0	0	0	0	0	2
S. Mbandaka	20	1	11	4	2	10	4	6
S. Rissen	20	0	0	5	0	7	5	4
S. Anatum	19	1	5	9	4	5	1	7
S. Livingstone	19	0	5	5	1	10	4	6
S. Heidelberg	20	2	2	1	3	3	0	6
S. Ohio	18	1	5	6	0	3	2	6
S. Kottbus	18	0	4	2	9	1	2	6
S. Dublin[c]	16	1	0	2	0	1	14	5

(a) n(TESSy)=27; n(FBO)=22; n(Broilers)=29; n(Pork)=26; n(Turkey)=26; n(Layers)=28; n(Cattle)=27.
(b) FBO: Foodborne outbreaks.
(c) Not included in the source attribution model.

Table C2. Number of serovars present in each country by data source.

Country	Number of serovars (n=25)						
	TESSy	FBO[a]	Broilers	Pork	Turkey	Layers	Cattle[b]
FR	25	9	10	14	9	17	1
BE	25	2	10	8	3	11	2
IT	25	0	9	10	8	16	4
DE	25	6	7	12	9	11	5
NL	25	2	6	9	6	2	4
UK	25	0	6	0	6	7	2
SK	25	2	5	7	1	1	0
AT	25	2	5	5	6	11	3
SE	25	2	1	2	0	2	4
DK	25	4	0	8	0	3	1
FI	25	4	0	0	0	1	2
CZ	24	1	7	7	6	3	6
HU	24	4	3	11	12	11	1
LU	24	0	0	5	0	0	2
IE	23	3	1	6	4	0	3
SI	22	1	3	10	9	4	1
LT	19	1	3	2	2	0	0
CY	18	0	6	8	1	4	-
EE	18	1	0	2	0	1	2
ES	13	0	9	14	10	19	3
RO[b]	13	2	4	-	-	4	3
PL	11	7	10	11	11	13	0
GR	10	0	11	13	2	5	0
MT[b]	10	-	6	-	-	-	-
LV	9	4	1	4	0	3	0
BG	-	-	6	3	0	0	3
PT	11	2	4	12	2	13	0
CH[b]	-	2	4	-	-	1	0
NO[b]	25	1	0	0	0	0	1

(a) FBO: Foodborne outbreaks;
(b) Not included in the source attribution model.

C(a). Animal data

Data was available from 28 countries in different combinations of animal data sources. Highest positivity at EU level was observed for turkeys (20.7%), followed by pigs (13.9%), broilers (13.1%), laying hens (5.9%) and bovine cattle (4.5%). However, given the non-uniformity of the data collection for bovines, interpretation of these estimates should be made with care. Belgium and the United Kingdom only reported positive samples for cattle, resulting in 100% positivity.

Small samples were also observed for broilers in Luxembourg, laying hens in Lithuania and Luxembourg, and turkeys in Estonia, Luxembourg and Latvia. These small samples showed a very low or, in most cases, zero positivity, which could be due to low representativeness. The total number of tested and positive units in each animal data source is presented in Table C3.

In broiler carcasses, *S.* Enteritidis was isolated in 15 out of 23 countries where positive broiler samples were detected. *S.* Infantis was observed in 15 countries, and *S.* Typhimurium in 10. Serovar predominance varied between countries: for example, in the Czech Republic, Lithuania and Sweden, *S.* Agona predominated, while *S.* Kentucky was the most frequent serovar in Ireland, Malta and the United Kingdom.

In pigs, *S.* Typhimurium was observed in all countries with positive samples, followed by *S.* Derby and *S.* Enteritidis, which occurred in 19 and 20 out of the 23 countries, respectively. Those were also the serovars observed in larger proportions in the countries where they occurred.

In turkeys, *S.* Typhimurium, *S.* Derby and *S.* Hadar prevailed among the 11 selected serovars, with the exception of Slovenia and Hungary, where *S.* Infantis and *S.* Enteritidis were more frequent. However, most positives were among serovars aggregated as "Others", due to the predominance of *S.* Saintpaul and *S.* Kottbus in this reservoir.

In layers, *S.* Enteritidis was present in 17 out of 22 countries, being the most frequent serovar in the majority of countries where it was detected. Finland, Luxembourg and Sweden were exceptions, with a predominance of *S.* Typhimurium. However, this could be due to a very small number of positive samples (one, one and five, respectively), the same occurring with *S.* Derby in Ireland (one out of two positives).

In cattle, S. Typhimurium was observed in large proportions in 12 out of 22 countries, although serovars grouped as "Other" were dominant in this source.

Overall, *S.* Enteritidis and *S.* Typhimurium were the most frequent and widespread serovars in animal reservoirs, followed by *S.* Infantis, *S.* Hadar and *S.* Derby. An exception can be noted for turkeys, where *S.* Saintpaul and *S.* Kottbus were more frequently isolated. *S.* Stanley was absent in all five sources. The relative proportion of the 11 selected serovars in the five animal sources is illustrated in Figures C1 to C5.

Table C3: Number of sampling units submitted and positivity percentages in animal reservoirs in the EU and Norway.

Country	Broiler carcasses[(a)]			Pigs – lymph node			Laying hen flocks			Turkeys – fattening flocks			Bovine cattle [(b)]		
	Submitted	Positives		Submitted	Positives		Submitted	Positives		Submitted	Positives		Submitted	Positives	
		n	%		n	%		N	%		N	%		N	%
AT	408	10	2.5	617	13	2.1	1,966	49	2.5	1,010	141	14.0	3,037	12	0.4
BE	380	77	20.3	601	78	13.0	649	76	11.7	370	40	10.8	81	81	100.0
BG	316	85	26.9	176	35	19.9	119	0	0.0	85	0	0.0	477	3	0.6
CY	357	38	10.7	359	47	13.1	40	5	12.5	70	28	40.0	-	-	-
CZ	422	23	5.5	654	38	5.8	449	40	8.9	970	192	19.8	696	24	3.4
DE	432	76	17.6	2,567	325	12.7	6304	220	3.5	1,475	108	7.3	4,053	163	4.0
DK	396	0	0.0	998	80	8.0	508	3	0.6	294	1	0.3	7,915	9	0.1
EE	102	0	0.0	420	27	6.4	52	4	7.7	2	0	0.0	1,550	10	0.6
ES	389	58	14.9	2,621	806	30.7	845	376	44.5	1,910	747	39.1	258	29	11.2
FI	369	0	0.0	419	0	0.0	950	1	0.1	675	0	0.0	3,415	7	0.2
FR	422	32	7.6	1,163	215	18.5	3067	187	6.1	1,630	157	9.6	-	-	2.4
GR	1,215	180	14.8	345	73	21.2	112	35	31.3	220	16	7.3	56	1	1.8
HU	321	275	85.7	656	75	11.6	866	101	11.7	1,465	915	62.5	178	31	17.4
IE	394	39	9.9	422	65	15.4	204	2	0.98	1,295	294	22.7	10,121	430	4.2
IT	393	66	16.8	709	116	16.4	821	171	20.8	1,370	277	20.2	1,797	17	0.9
LT	374	26	6.9	461	8	1.7	13	0	0.0	315	14	4.4	172	2	1.2
LU	13	0	0.0	313	50	16.0	7	1	14.3	1	0	0.0	83	7	8.4
LV	122	6	4.9	392	21	5.4	69	14	20.3	1	0	0.0	25	0	0.0
MT	367	77	21,0	-	-	-	-	-	-	-	-	-	-	-	-
NL	429	43	10.0	1,087	92	8.5	2346	62	2.6	860	77	9.0	330	18	5.5
PL	419	107	25.5	1,176	75	6.4	1533	192	12.5	1,610	285	17.7	130	0	0.0
PT	421	47	11.2	658	156	23.7	227	83	36.56	525	26	5.0	56	0	0.0
RO	357	17	4.8	-	-	-	-	-	-	-	-	-	521	3	0.6
SE	410	1	0.2	394	6	1.5	724	5	0.7	70	0	0.0	3,728	60	1.6
SI	413	7	1.7	431	27	6.3	172	18	10.5	655	100	15.3	386	1	0.3
SK	422	91	21.6	385	30	7.8	138	10	7.2	125	15	12.0	95	0	0.0
UK	401	14	3.5	639	139	21.8	5523	67	1.2	1,570	401	25.5	895	895	100.0
EU Total	9,249	1,215	13.1	18,663	2,596	13.9	27,704	1630	5.9	18,514	3,834	20.7	40,055	1,803	4.5
NO	396	0	0.0	408	1	0.2	1080	0	0.0	360	0	0.0	2,589	1	0.0
Total	10,035	1,225	12.2	19,072	2,598	13.6	28,784	1630	5.7	18,849	3,834	20.3	42,644	1,804	4.2

(a) In the specific case of Greece, broiler flocks.
(b) In the specific case of Denmark, carcass samples collected at the slaughterhouse.

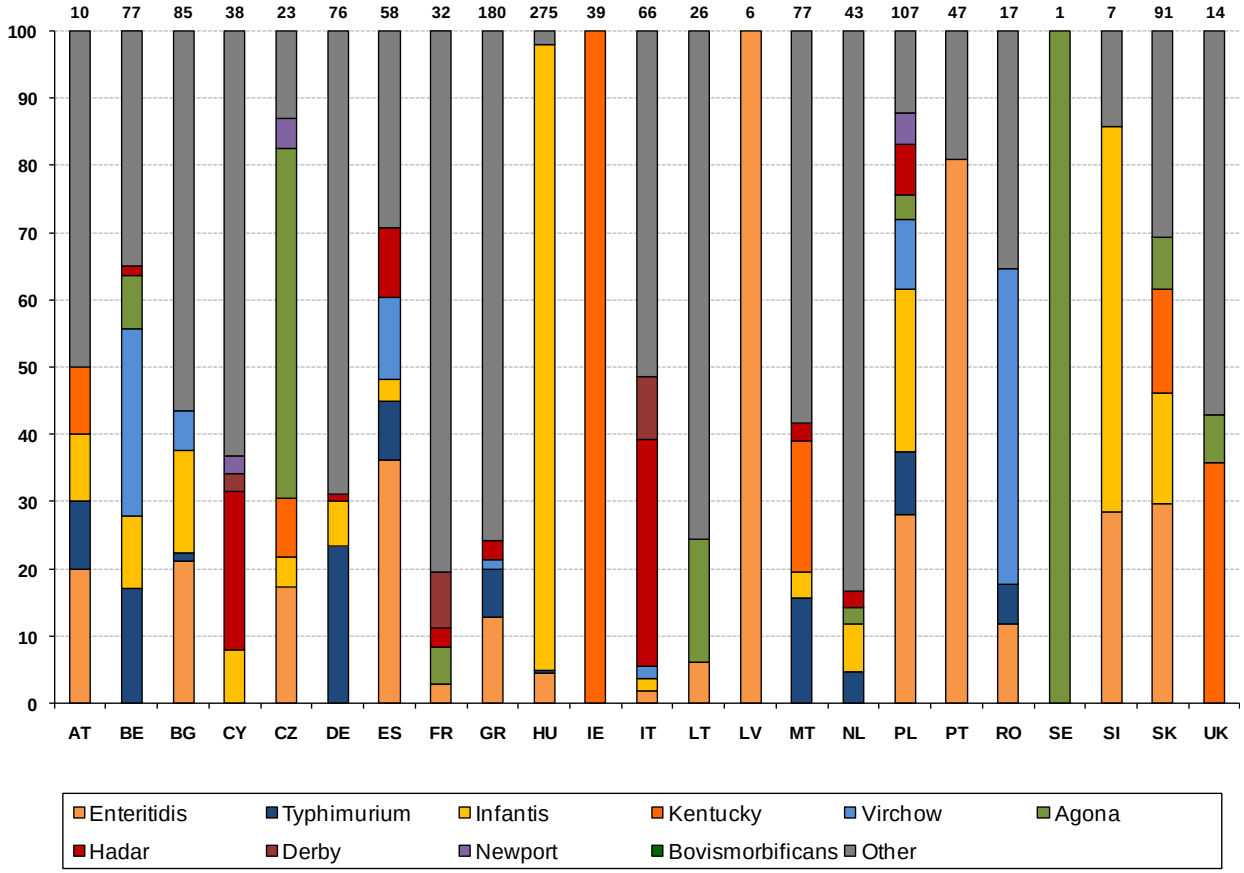


Figure C1: Relative frequency of selected *Salmonella* serovars on broiler carcasses. The number of positive samples is shown at the top of the bars.

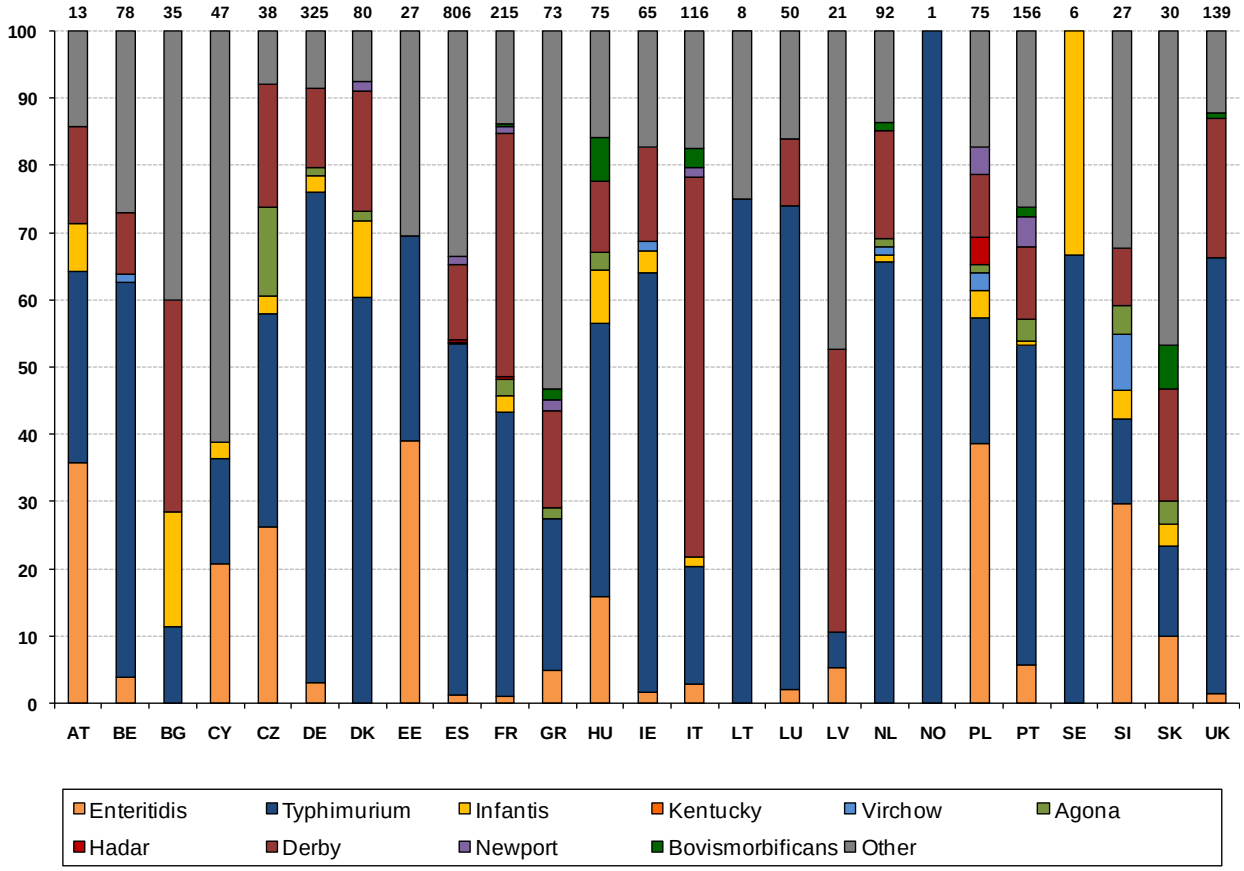


Figure C2**:** Relative frequency of selected *Salmonella* serovars in pigs. The number of positive samples is shown at the top of the bars.

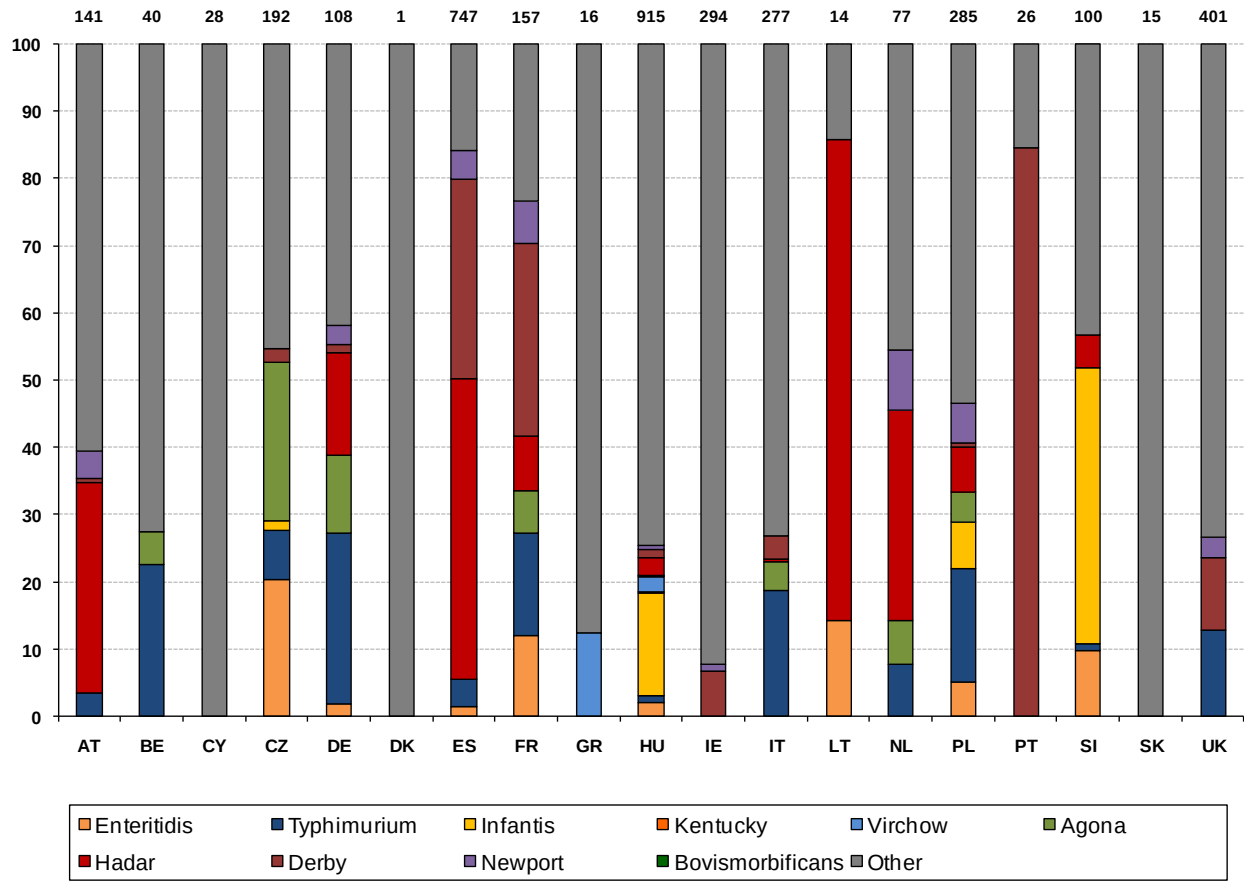


Figure C3: Relative frequency of selected *Salmonella* serovars in turkeys. The number of positive samples is shown at the top of the bars.

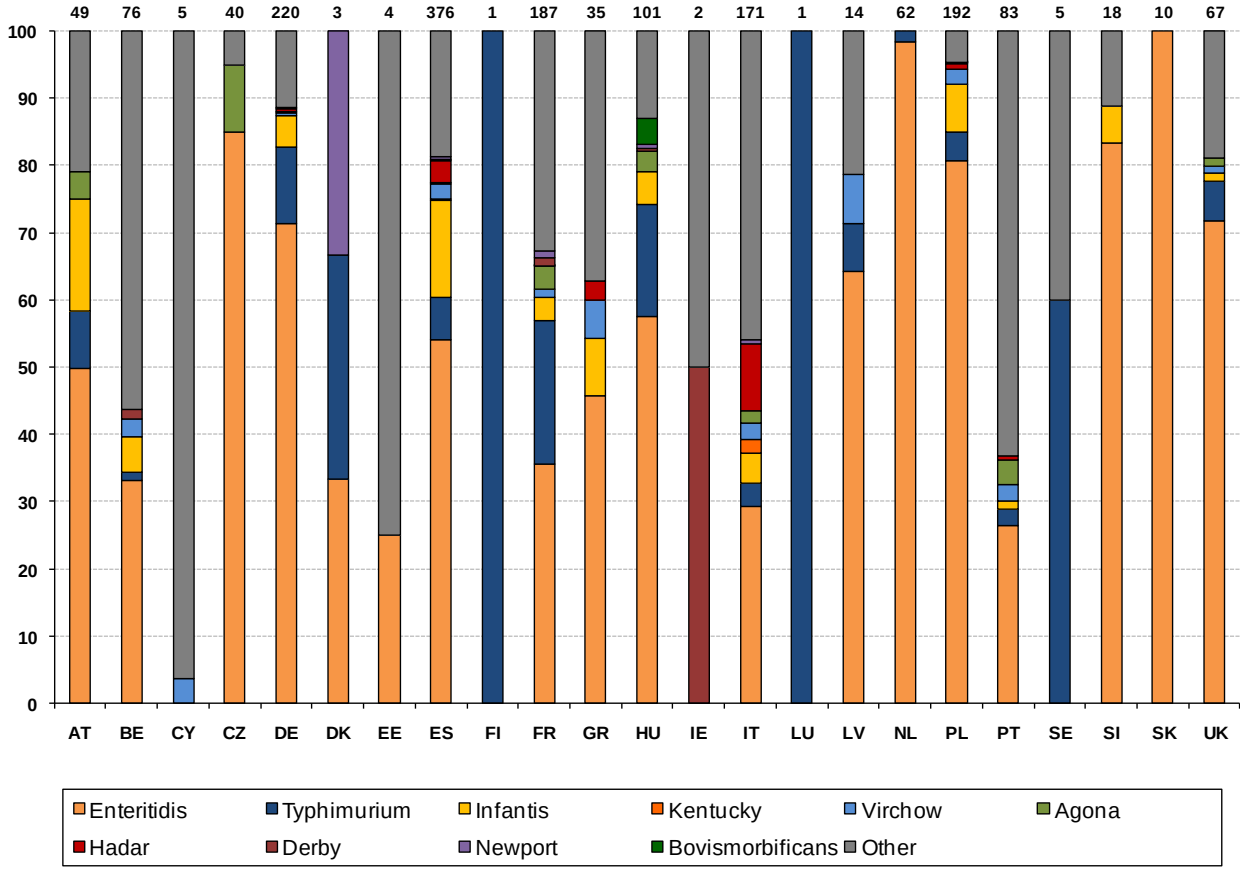


Figure C4: Relative frequency of selected *Salmonella* serovars in laying hens. The number of positive samples is shown at the top of the bars.

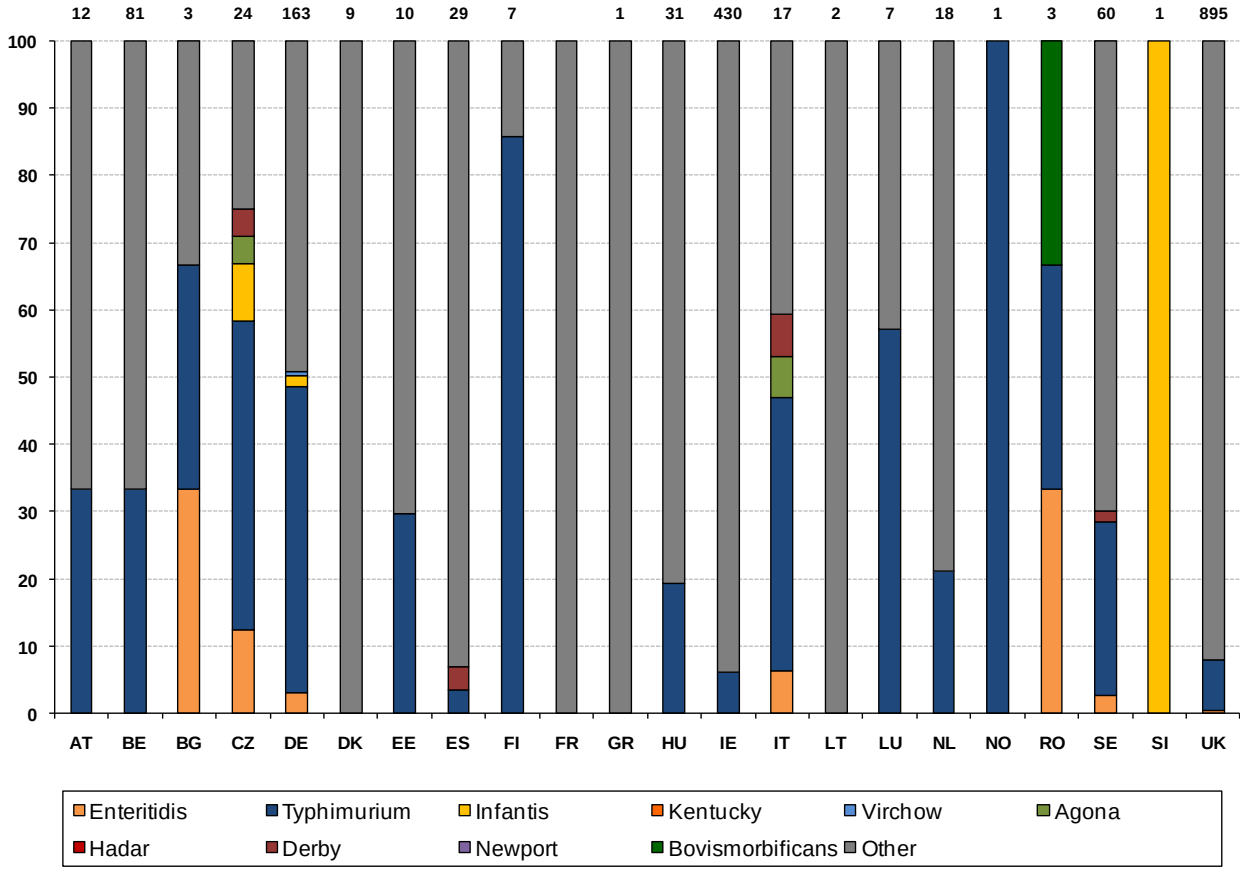


Figure C5: Relative frequency of selected *Salmonella* serovars in cattle. The number of positive samples is shown at the top of the bars.

C(b). Human data

A total of 392,485 *Salmonella* cases were reported in the EU in the study period (2007-2009), with 19,835 related to outbreaks and 35,682 reported as acquired outside the country of reporting. The resulting incidence at EU level over the three years was 77 per 100,000 inhabitants. Country-specific incidences were calculated, but should be considered carefully, as different degrees of underreporting are expected in each MS. The percentage of non-serotyped cases reassigned to specific serovars in the EU was 9.1%, varying from zero in Portugal to 84.4% in Romania. The number of cases, and the outbreak- and travel-related cases included in the model, as well as the total number of cases as reported in the CSR is presented in Table C4.

S. Enteritidis was the most widely and frequently reported serovar, followed by S. Typhimurium and S. Virchow. However, other serovars predominated in specific countries, particularly in outbreaks, such as S. Newport in Finland and S. Stanley in Sweden (here included in "Other"). The relative proportions of the 11 selected serovars in cases reported to TESSy and among outbreak cases can be observed in Figure C6. Bulgaria was not included in this graph because there was no serovar information available.

The geographical distribution of the incidences of 11 selected serovars in the EU MSs included in this report and Norway are shown in Figures C7 to C17.

Table C4: Reported and outbreak-related cases of *Salmonella* in humans in the EU, Norway and Switzerland, 2007-2009.

Country	TESSy[a]	Travel	Outbreaks	Reassigned[b]		CSR	Incidence (2007-2009)	Population[c]
				n	%		(/1/100,000)	(/1,000)
AT	8,487	988	421	783	9.2	8,460	101	8,337
BE	11,066	0	91	172	1.6	10,917	103	10,590
BG	3,899	-	-	-	-	3,899	51	7,693
CY	471	18	0	112	23.8	461	53	862
CZ	38,842	657	337	586	1.5	39,032	378	10,319
DE	127,330	6,683	2,383	15,929	12.5	129,704	158	82,264
DK	7,497	1,366	2,224	372	5.0	7,461	137	5,458
EE	1,341	95	157	53	4.0	1,338	100	1,341
ES	12,033	0	469	4,595	38.2	12,419	28	44,486
FI	8,228	6,845	189	73	0.9	8,228	155	5,304
FR	20,319	0	2,609	2,185	10.8	19,849	32	62,036
GR[d]	1,927	45	0	1,416	73.5	2,154	19	11,137
HU	19,091	29	1,921	1,158	6.1	19,244	192	10,012
IE	1,264	384	67	83	6.6	1,223	28	4,437
IT	10,205	132	0	1,111	10.9	11,887	20	59,604
LT	7,643	21	371	403	5.3	7,641	230	3,321
LU	479	46	0	63	13.2	527	110	481
LV	2,665	32	512	661	24.8	2,664	118	2,261
MT	371	4	0	60	16.2	370	91	407
NL	4,168	497	700	294	7.1	4,077	25	16,528
PL	30,963	16	5,310	1,204	3.9	29,268	77	38,104
PT	1,513	5	90	0	0.0	1,036	10	10,677
RO[d]	2,351	0	437	1,984	84.4	2,359	11	21,532
SE	11,265	8,752	272	786	7.0	11,169	121	9,205
SI	3,002	0	692	63	2.1	2,995	149	2,015
SK	19,399	146	583	328	1.7	15,879	294	5,400
UK	36,666	8,921	0	1,169	3.2	35,972	59	61,231
EU total	392,485	35,682	19,835	35,643	9.1	390,233	77	495,040

CH	-	-	6	-	-	5,178	69	7,455
NO	4,825	3,721	95	31	0.8	4,825	101	4,767
Total	397,310	39,403	19,936	35,674	9.0	400,236	79	507,262

(a) For Poland and Portugal, data provided directly by Member states.
(b) Units not typed, with incomplete typing or aggregated as serogroups and "Others".
(c) WHO, 2011; Human population as reported in 2009.
(d) Large proportion of data with no serovar detailing, so mapped incidences per serovar should appear smaller than expected from this value.

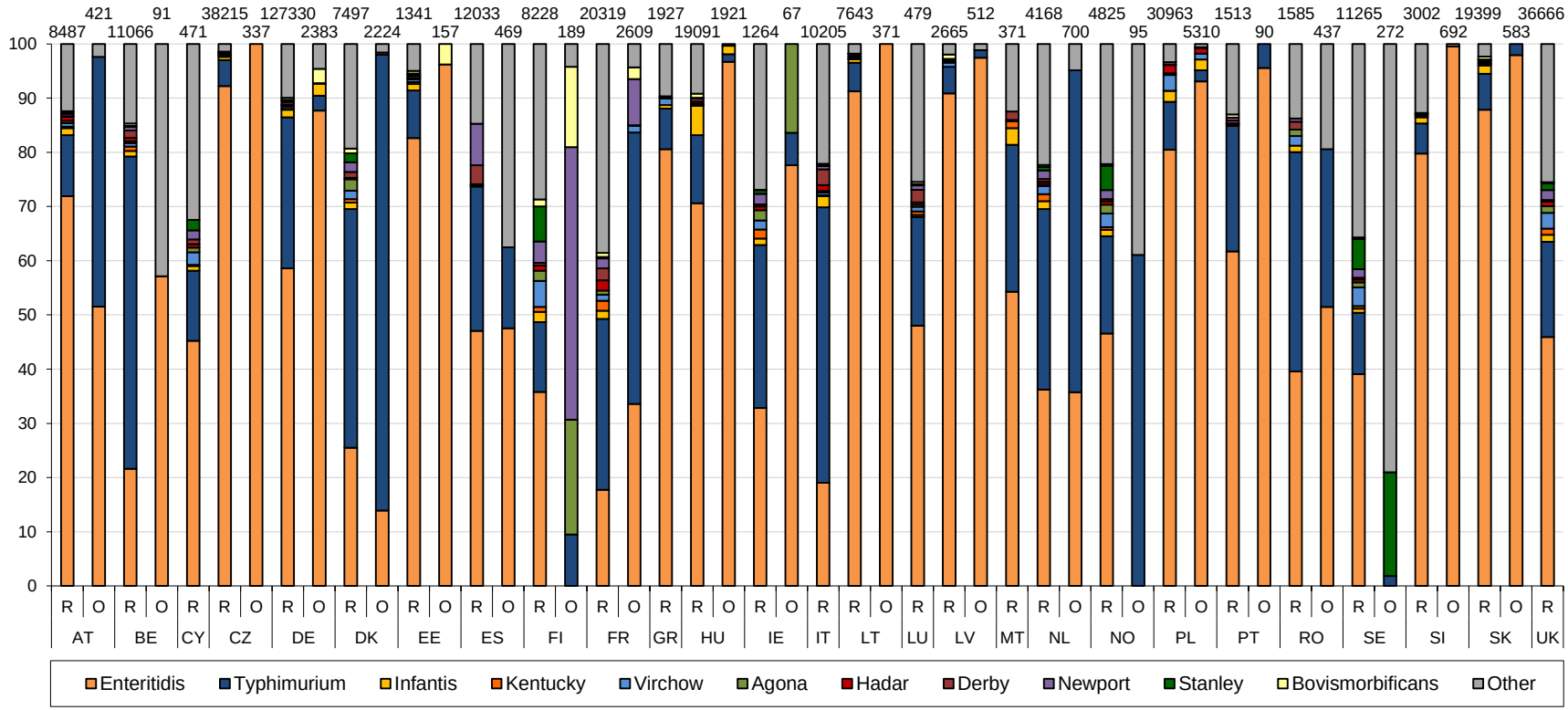


Figure C6: Relative proportions of selected serovars in total reported (R) and outbreak (O) cases in humans in the EU and Norway, 2007-2009. The totals for each country in the datasets are shown at the top of the bar.

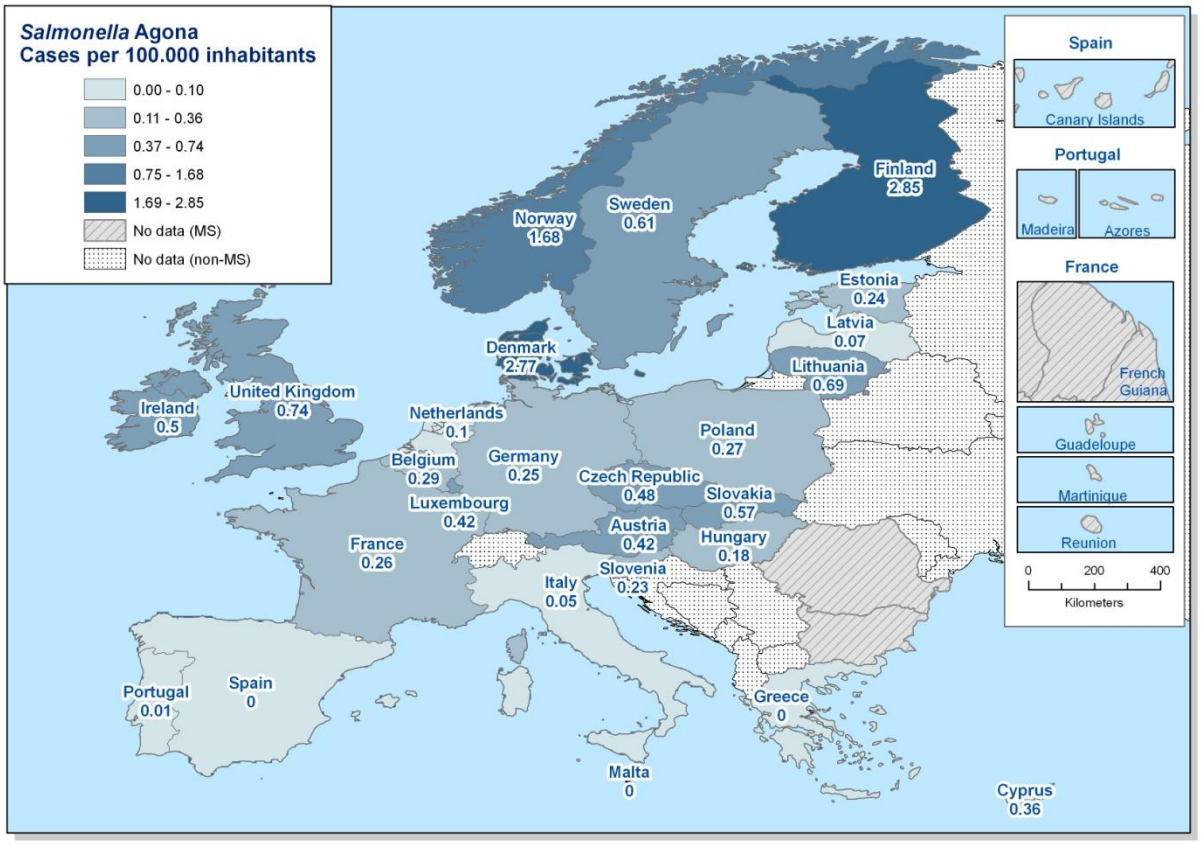


Figure C7: Incidence of *S.* Agona in EU countries and Norway, 2007-2009.

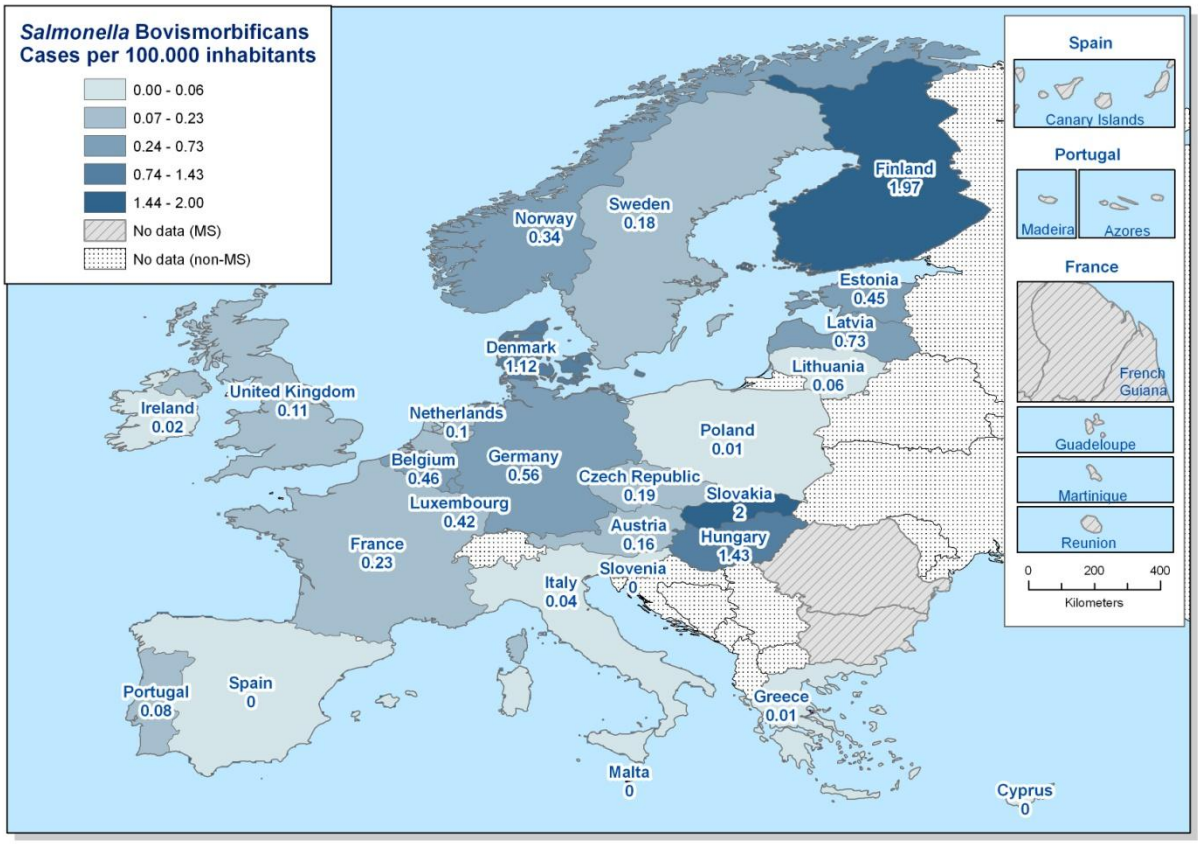


Figure C8: Incidence of *S.* Bovismorbificans in EU countries and Norway, 2007-2009.

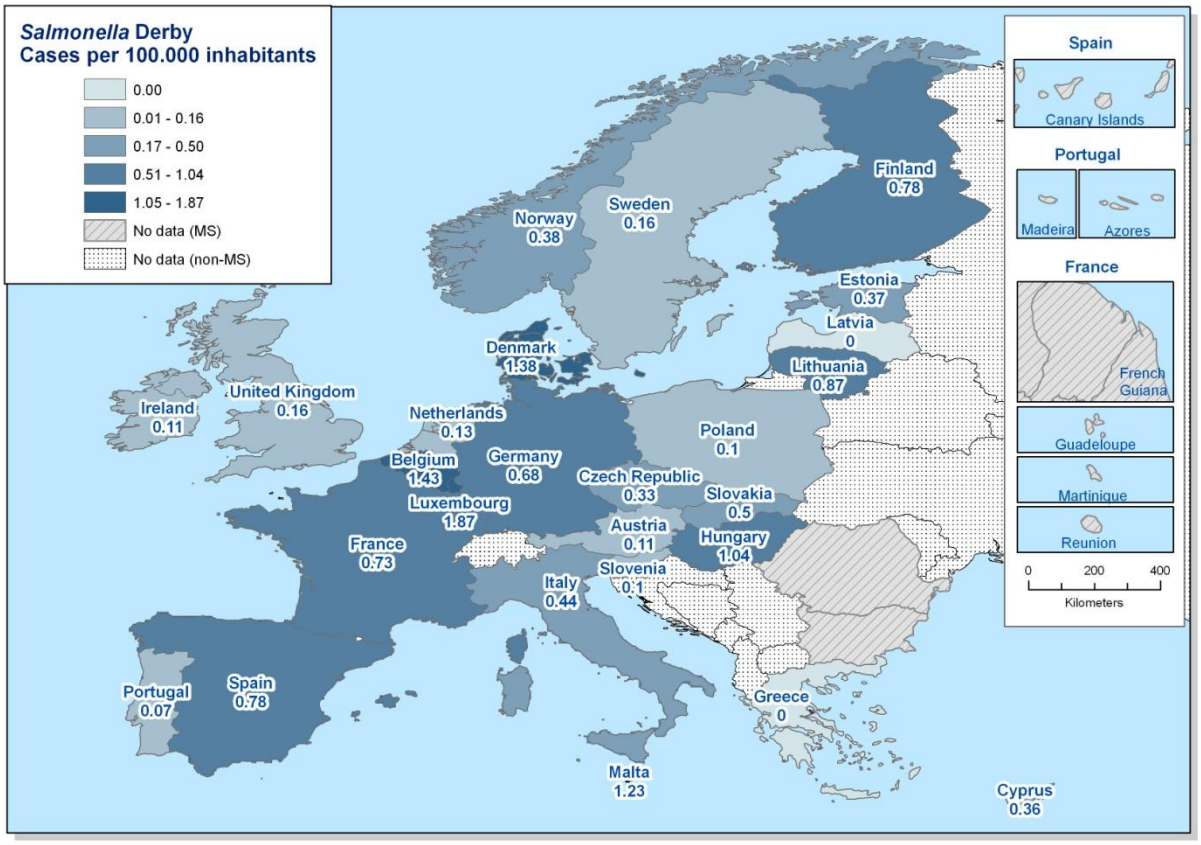


Figure C9: Incidence of *S.* Derby in EU countries and Norway, 2007-2009.

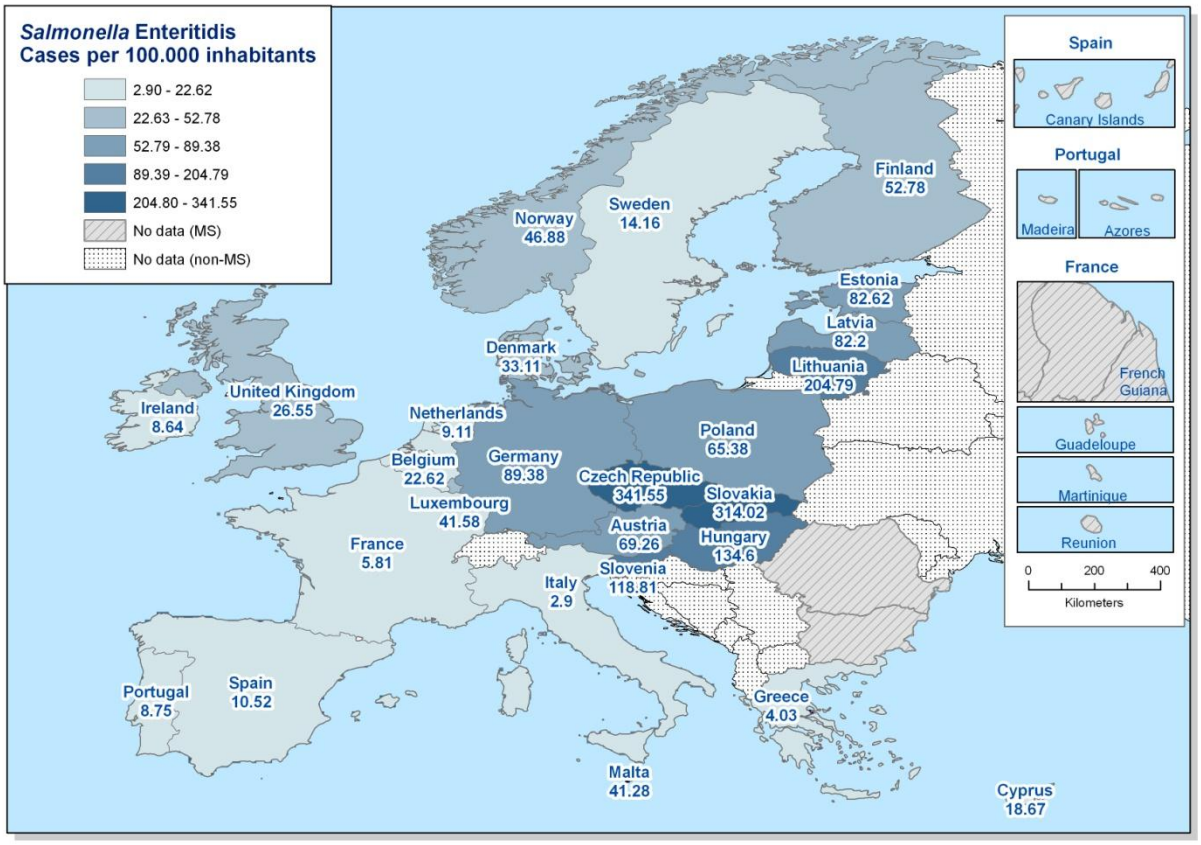


Figure C10: Incidence of *S.* Enteritidis in EU countries and Norway, 2007-2009.

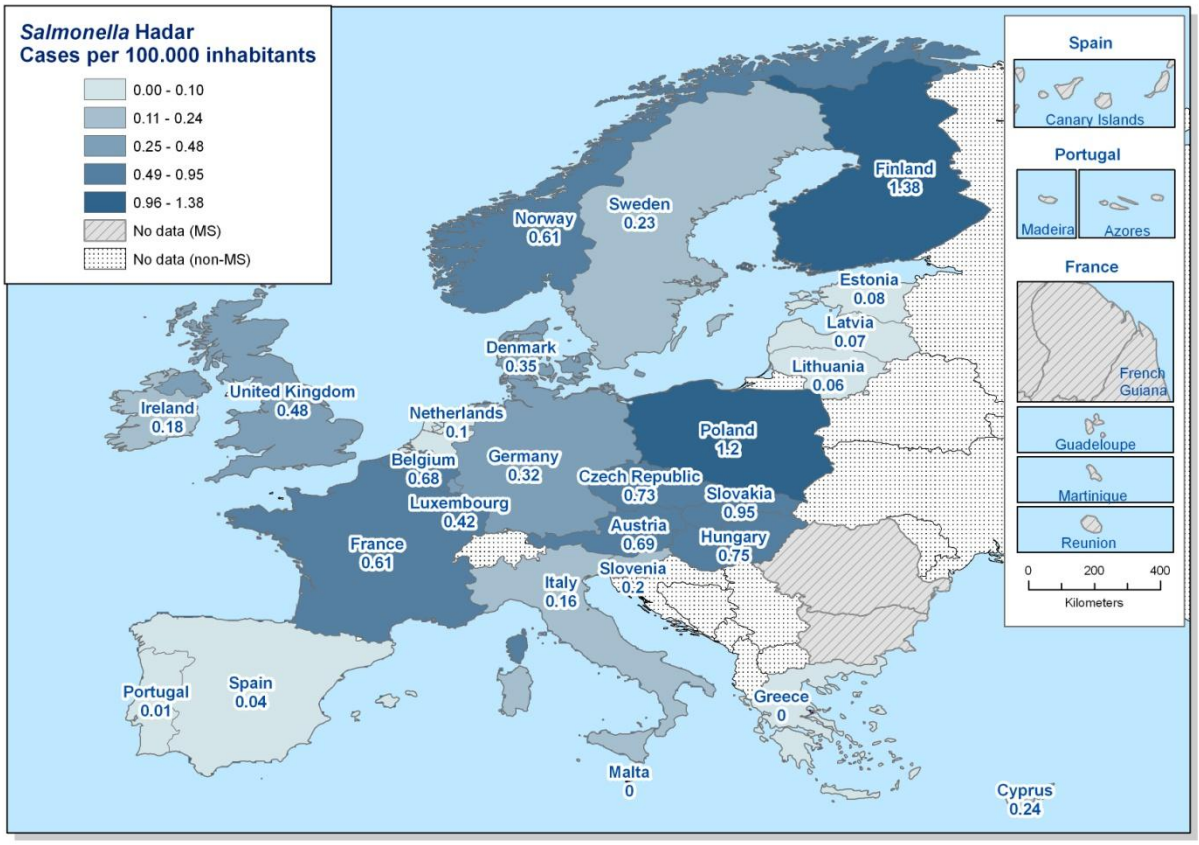


Figure C11: Incidence of *S.* Hadar in EU countries and Norway, 2007-2009.

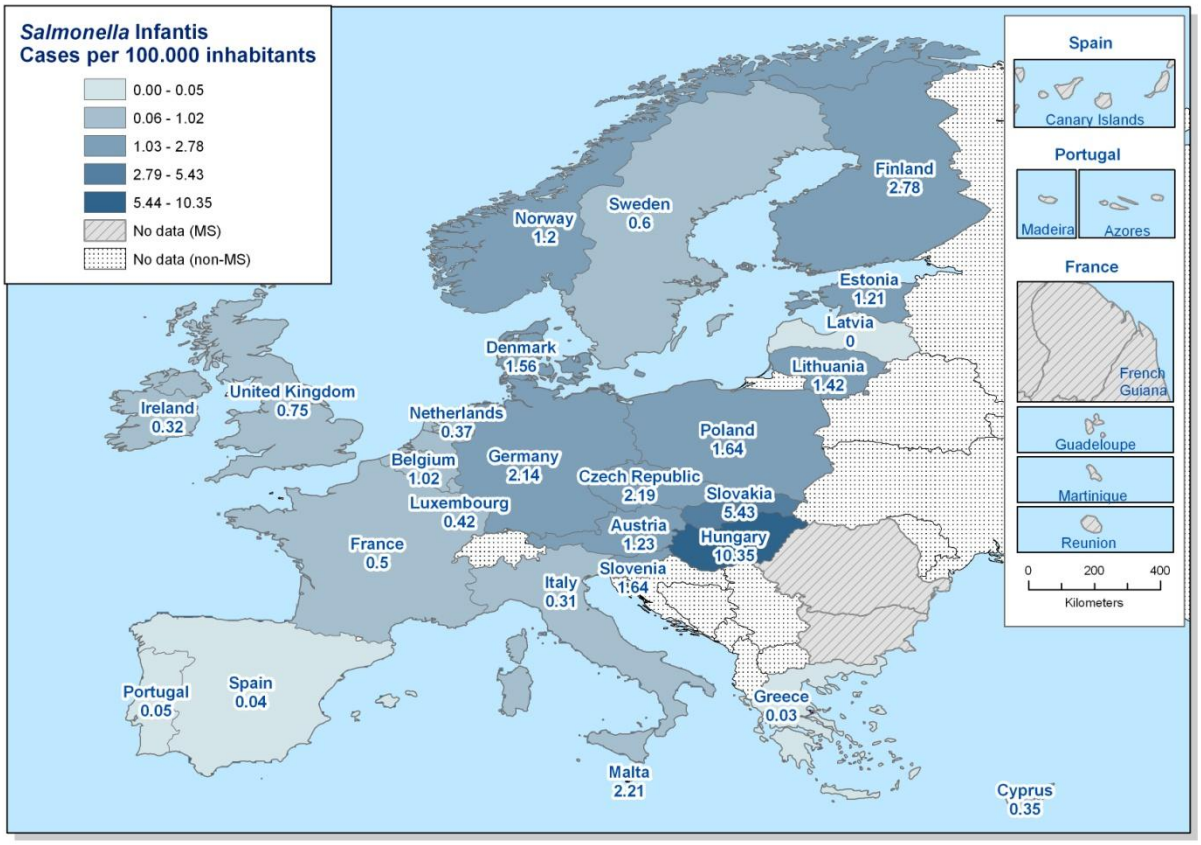


Figure C12: Incidence of *S.* Infantis in EU countries and Norway, 2007-2009.

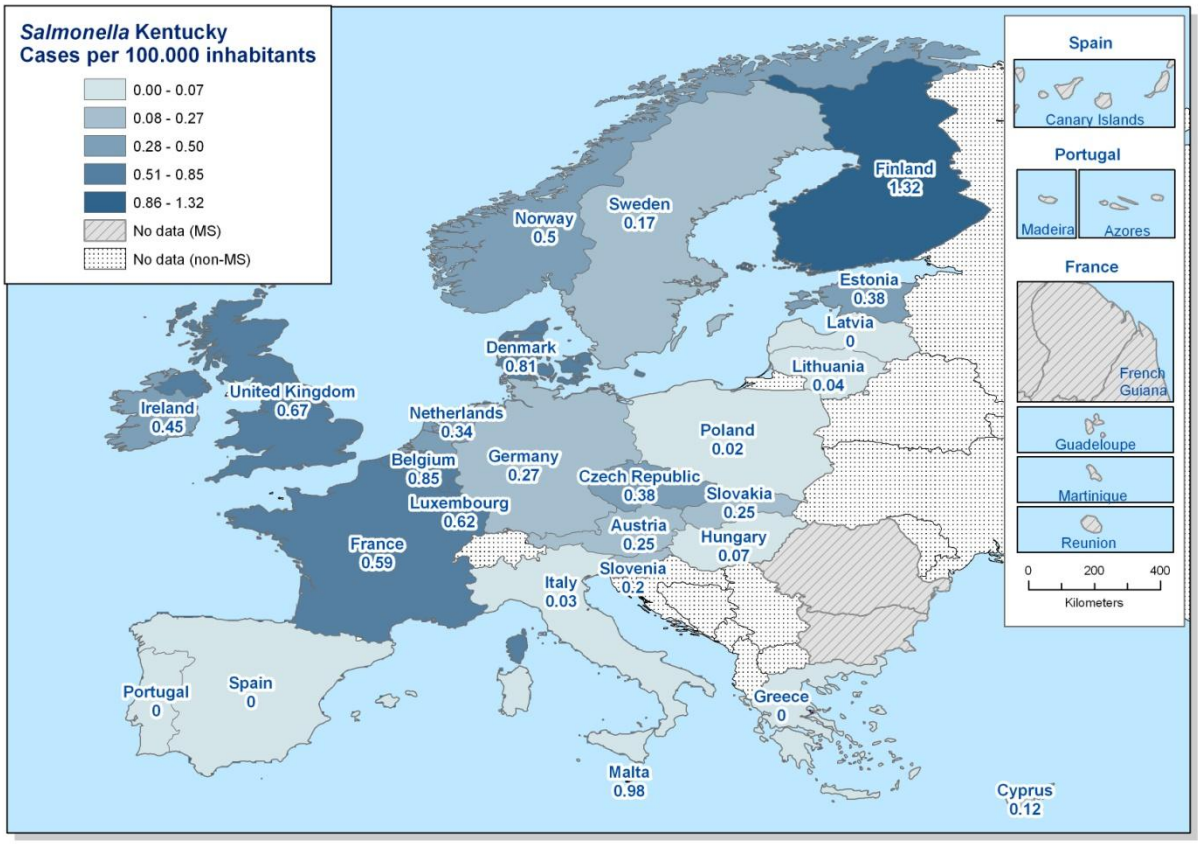


Figure C13: Incidence of *S.* Kentucky in EU countries and Norway, 2007-2009.

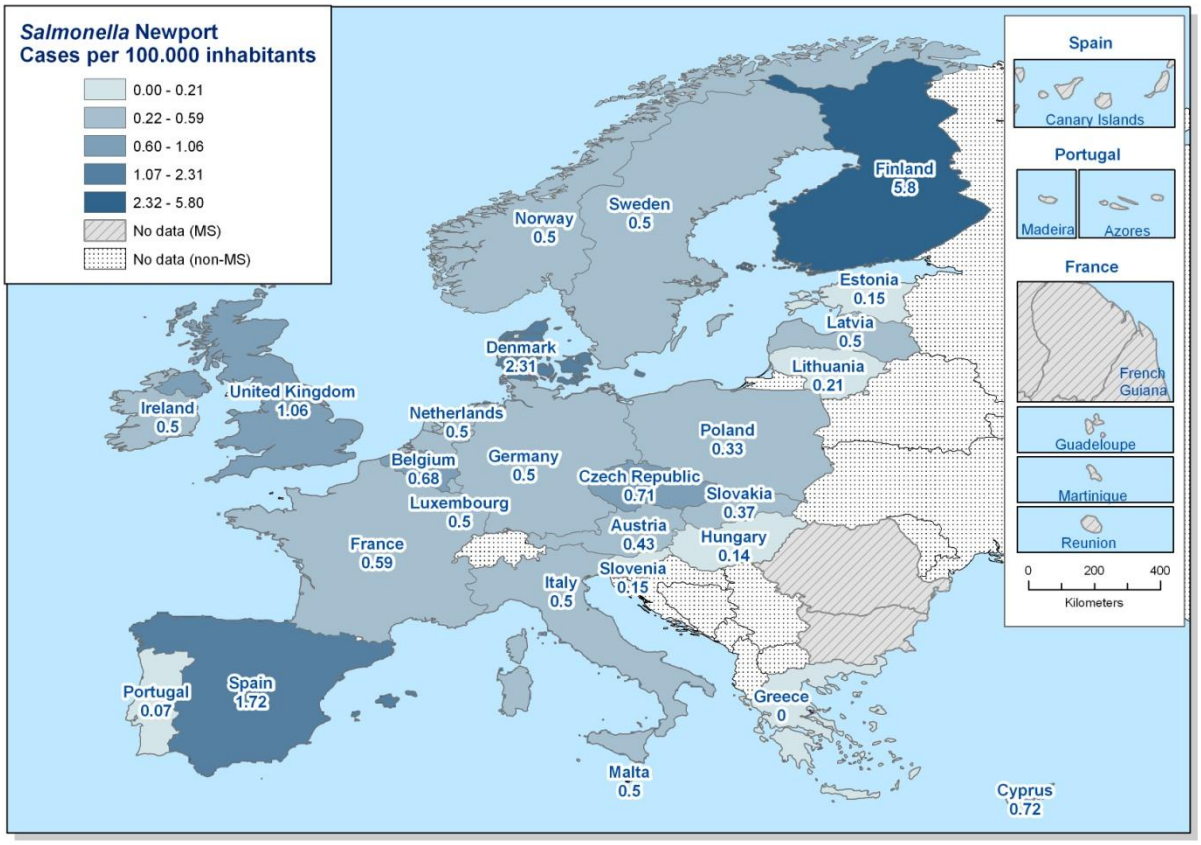


Figure C14: Incidence of *S.* Newport in EU countries and Norway, 2007-2009.

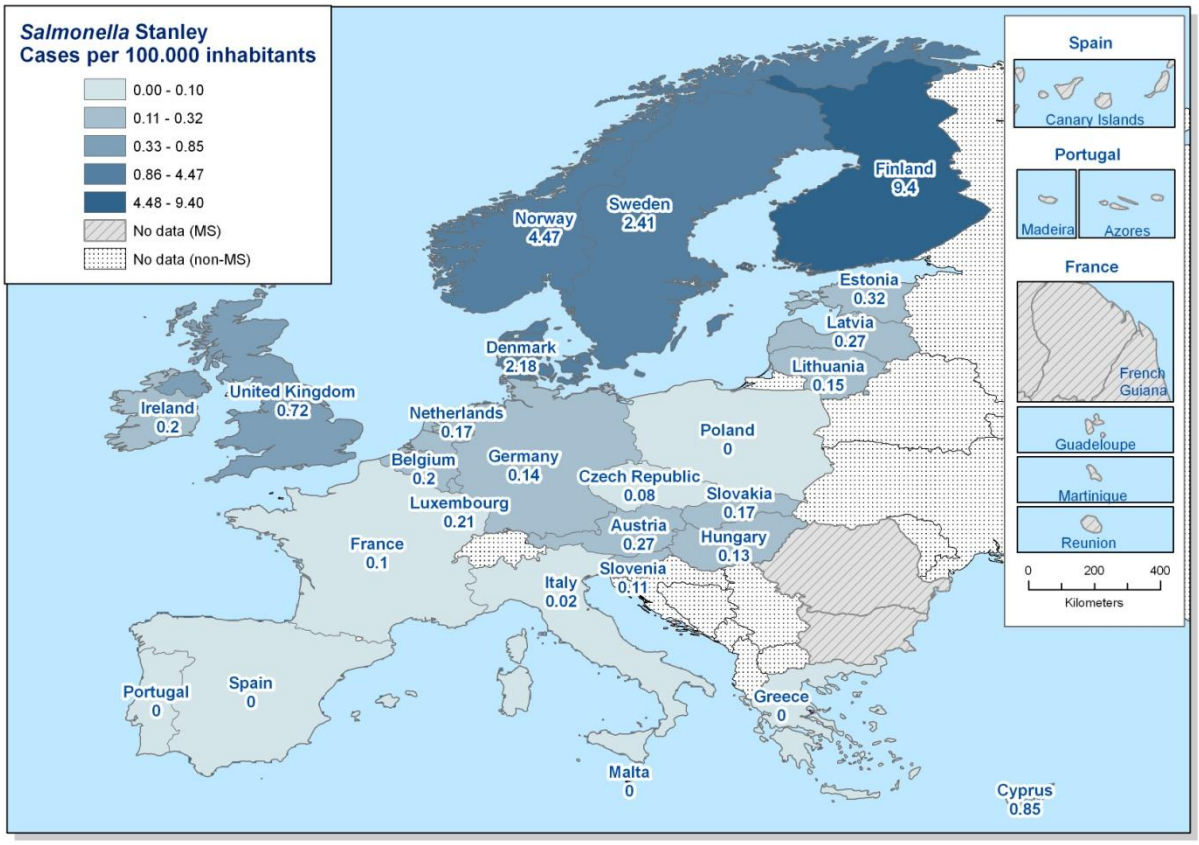


Figure C15: Incidence of *S.* Stanley in EU countries and Norway, 2007-2009.

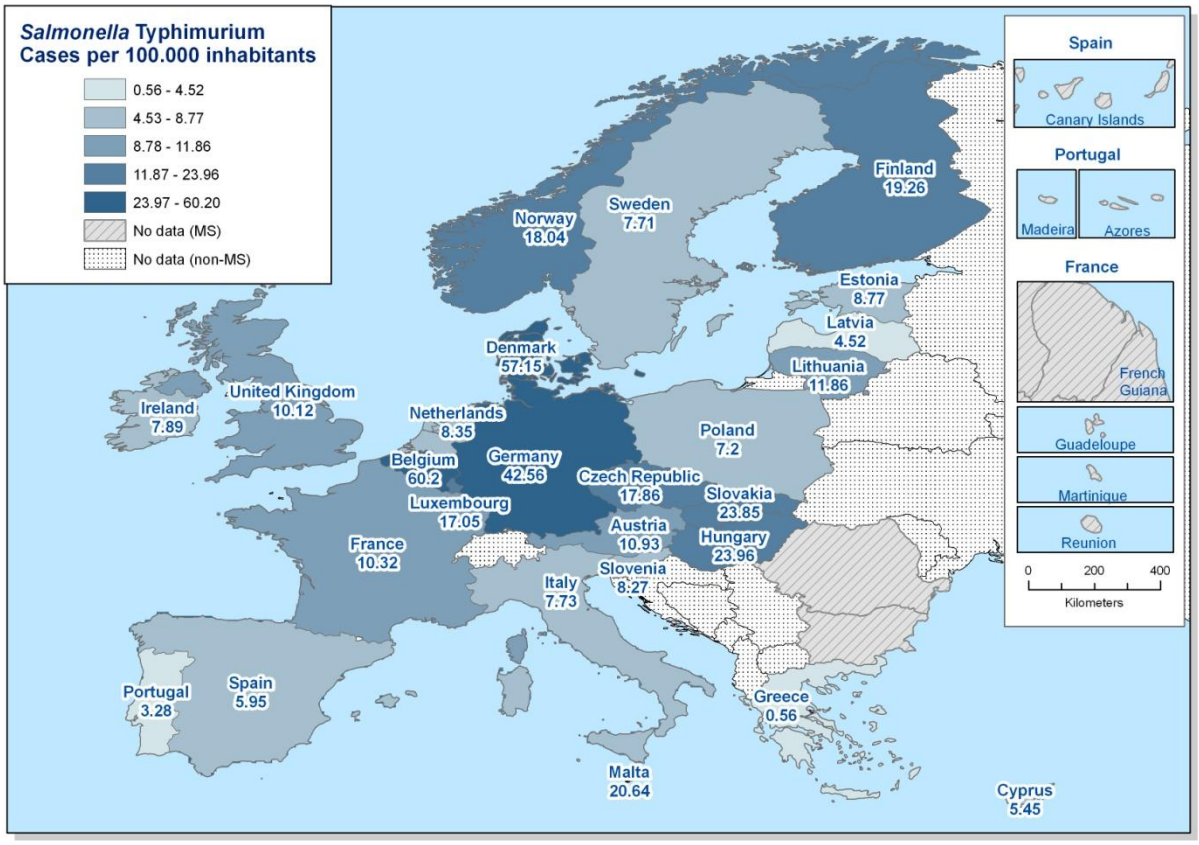


Figure C16: Incidence of *S.* Typhimurium in EU countries and Norway, 2007-2009.

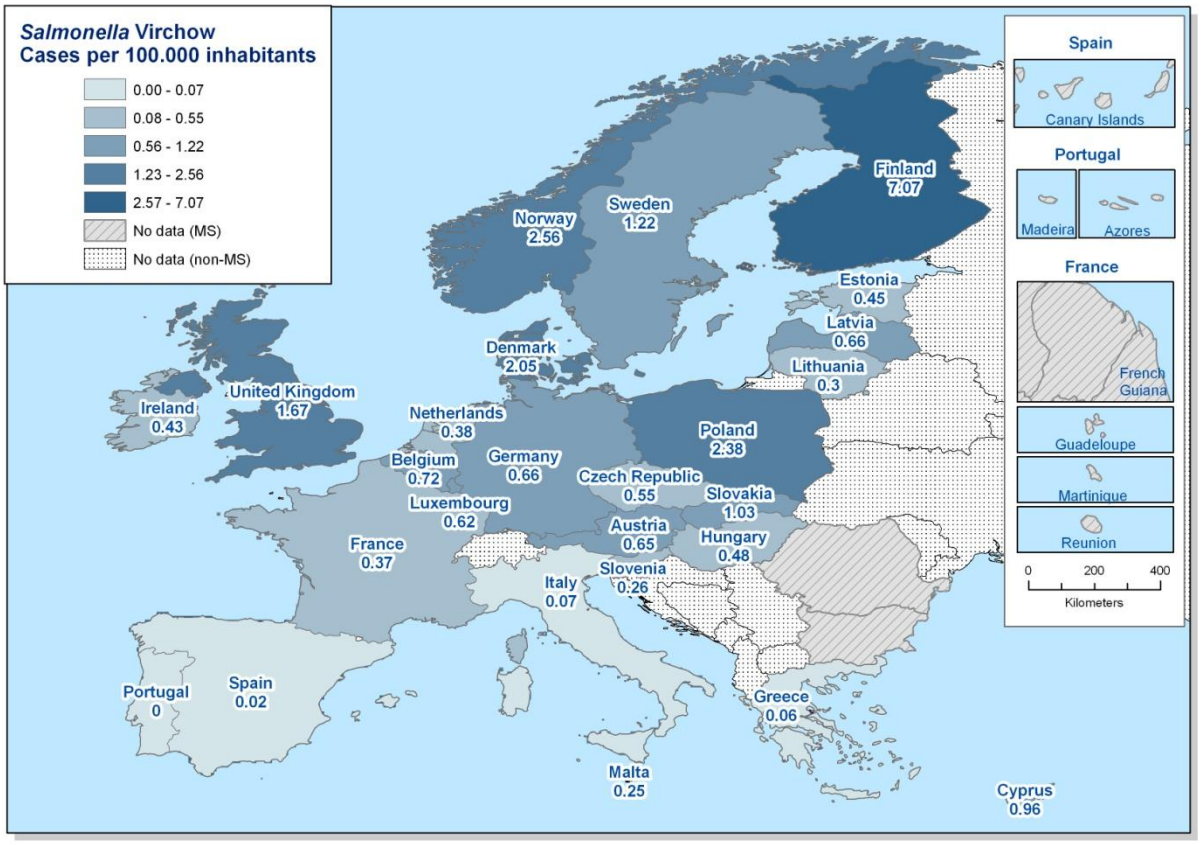


Figure C17: Incidence of *S.* Virchow in EU countries and Norway, 2007-2009.

APPENDIX D. SOURCE ATTRIBUTION ESTIMATES FOR 24 MEMBER STATES BY REPORTING COUNTRIES

Table D1. Proportion of human *Salmonella* cases attributed to food-animal reservoirs, travel-related, outbreak- related and with unknown source in Austria (AT), Belgium (BE) and Cyprus (CY), 2007-2009 (median % and 95% Credibility Interval).

	AT			BE			CY		
Source	**%**	**95% CI**	**Total**	**%**	**95% CI**	**Total**	**%**	**95% CI**	**Total**
Broilers	0.0	[0.0, 0.2]	0.3	2.3	[1.8, 2.8]	2.3	4.8	[2.4, 7.8]	4.8
Pigs	13.8	[12.1, 15.4]	13.8	73.7	[71.7, 75.7]	74.0	51.3	[42.8, 60.0]	51.3
Turkeys	3.6	[2.8, 4.5]	3.6	9.2	[8.0, 10.5]	9.2	6.3	[2.2, 11.6]	6.3
Layers	57.0	[54.8, 59.2]	58.5	2.9	[1.7, 4.1]	2.9	8.7	[4.2, 14.6]	8.7
Travel	11.6		11.6	0.0		0.0	3.8		3.8
Unknown	9.0	[7.1, 11.0]	9.0	11.2	[9.4, 12.9]	11.2	25.1	[17.1, 32.6]	25.1
Outbreak	5.0		3.2	0.8		0.5	0.0		0.0

Total: Includes sporadic cases and outbreak-related cases attributed to the responsible source where this was reported.

Table D2. Proportion of human *Salmonella* cases attributed to food-animal reservoirs, travel-related, outbreak- related and with unknown source in the Czech republic (CZ), Germany (DE) and Denmark (DK), 2007-2009 (median % and 95% Credibility Interval).

	CZ			DE			DK		
Source	**%**	**95% CI**	**Total**	**%**	**95% CI**	**Total**	**%**	**95% CI**	**Total**
Broilers	0.1	[0.0, 0.2]	0.1	0.5	[0.1, 0.9]	0.5	2.6	[1.4, 4.0]	2.8
Pigs	10.9	[10.2, 11.5]	10.9	32.5	[31.8, 33.1]	32.7	13.3	[11.8, 14.9]	15.6
Turkeys	1.7	[1.4, 2.1]	1.7	1.3	[1.1, 1.5]	1.3	15.1	[12.9, 17.4]	15.1
Layers	83.9	[82.8, 85.0]	84.6	51.1	[50.5, 51.7]	51.2	7.0	[5.5, 8.5]	10.5
Travel	1.7		1.7	5.2		5.2	18.2		18.2
Unknown	0.8	[-0.2, 1.8]	0.8	7.5	[7.0, 8.0]	7.5	14.1	[12.4, 15.7]	14.1
Outbreak	0.9		0.2	1.9		1.6	29.7		23.8

Total: Includes sporadic cases and outbreak-related cases attributed to the responsible source where this was reported.

Table D3. Proportion of human *Salmonella* cases attributed to food-animal reservoirs, travel-related, outbreak- related and with unknown source in Estonia (EE), Spain (ES) and Finland (FI), 2007-2009 (median % and 95% Credibility Interval).

	EE				ES				FI			
Source	**%**	**95% CI**		**Total**	**%**	**95% CI**		**Total**	**%**	**95% CI**		**Total**
Broilers	3.6	[0.7,	7.4]	10.6	0.1	[0.0,	0.5]	0.1	0.6	[0.0,	1.9]	0.6
Pigs	24.4	[18.7,	30.7]	24.4	31.8	[30.4,	33.3]	31.8	4.9	[3.5,	6.1]	4.9
Turkeys	1.8	[0.7,	3.6]	1.8	12.4	[11.0,	13.8]	12.4	1.7	[0.5,	3.1]	1.7
Layers	49.0	[42.9,	55.2]	49.0	41.5	[40.1,	42.9]	41.5	2.5	[1.1,	4.1]	2.5
Travel	7.1			7.1	0.0			0.0	83.2			83.2
Unknown	2.3	[-2.7,	7.1]	2.3	10.3	[8.6,	11.9]	10.3	4.8	[3.1,	6.4]	4.8
Outbreak	11.7			4.7	3.9			3.9	2.3			2.3

Total: Includes sporadic cases and outbreak-related cases attributed to the responsible source where this was reported.

Table D4. Proportion of human *Salmonella* cases attributed to food-animal reservoirs, travel-related, outbreak- related and with unknown source in France (FR), Greece (GR) and Hungary (HU), 2007-2009 (median % and 95% Credibility Interval).

	FR				GR				HU			
Source	**%**	**95% CI**		Total	**%**	**95% CI**		Total	**%**	**95% CI**		Total
Broilers	11.7	[10.9,	12.5]	12.8	0.8	[0.0,	4.3]	0.8	4.0	[3.5,	4.6]	4.2
Pigs	30.0	[29.0,	31.0]	32.5	9.5	[7.8,	11.3]	9.5	24.1	[22.4,	25.8]	24.3
Turkeys	11.1	[10.0,	12.1]	11.1	0.3	[0.0,	1.0]	0.3	4.9	[4.3,	5.5]	4.9
Layers	2.3	[1.8,	2.9]	6.9	78.6	[74.0,	83.0]	78.6	49.5	[47.7,	51.3]	49.7
Travel	0.0			0.0	2.3			2.3	0.2			0.2
Unknown	32.0	[31.0,	33.1]	32.0	8.3	[4.0,	12.5]	8.3	7.3	[6.0,	8.6]	7.3
Outbreak	12.8			4.8	0.0			0.0	10.1			9.5

Total: Includes sporadic cases and outbreak-related cases attributed to the responsible source where this was reported.

Table D5. Proportion of human *Salmonella* cases attributed to food-animal reservoirs, travel-related, outbreak- related and with unknown source in Ireland (IE), Italy (IT) and Lithuania (LT), 2007-2009 (median % and 95% Credibility Interval).

	IE			IT			LT		
Source	**%**	**95% CI**	**Total**	**%**	**95% CI**	**Total**	**%**	**95% CI**	**Total**
Broilers	1.4	[0.8, 2.3]	1.4	2.3	[1.9, 2.8]	2.3	1.1	[0.4, 1.9]	1.6
Pigs	26.0	[22.1, 30.1]	26.0	73.2	[71.0, 75.4]	73.2	9.1	[7.9, 10.3]	9.1
Turkeys	8.4	[5.7, 11.7]	8.4	5.3	[4.3, 6.4]	5.3	0.7	[0.3, 1.3]	0.7
Layers	13.9	[10.7, 17.3]	14.2	2.1	[1.3, 3.2]	2.1	82.8	[80.5, 85.2]	82.8
Travel	30.3		30.3	1.3		1.3	0.3		0.3
Unknown	14.7	[9.9, 19.2]	14.7	15.8	[14.0, 17.6]	15.8	1.2	[-1.0, 3.4]	1.2
Outbreak	5.3		5.0	0.0		0.0	4.9		4.4

Total: Includes sporadic cases and outbreak-related cases attributed to the responsible source where this was reported.

Table D6. Proportion of human *Salmonella* cases attributed to food-animal reservoirs, travel-related, outbreak- related and with unknown source in Luxembourg (LU), Latvia (LV) and the Netherlands (NL), 2007-2009 (median % and 95% Credibility Interval).

	LU			LV			NL		
Source	**%**	**95% CI**	Total	**%**	**95% CI**	Total	**%**	**95% CI**	Total
Broilers	4.3	[1.3, 8.7]	4.3	0.5	[0.0, 2.3]	3.5	3.8	[2.9, 5.0]	3.9
Pigs	8.4	[3.6, 14.5]	8.4	11.1	[9.2, 13.3]	12.2	22.9	[20.9, 24.8]	22.9
Turkeys	6.8	[3.4, 11.5]	6.8	0.2	[0.0, 0.7]	0.2	8.1	[6.5, 10.0]	8.1
Layers	50.0	[41.2, 59.1]	50.0	67.2	[63.5, 70.8]	69.2	21.7	[20.0, 23.5]	27.2
Travel	9.6		9.6	1.2		1.2	11.9		11.9
Unknown	20.9	[12.7, 28.6]	20.9	0.6	[-2.8, 3.9]	0.6	14.7	[12.2, 17.1]	14.7
Outbreak	0.0		0.0	19.2		13.2	16.8		11.3

Total: Includes sporadic cases and outbreak-related cases attributed to the responsible source where this was reported.

Table D7. Proportion of human *Salmonella* cases attributed to food-animal reservoirs, travel-related, outbreak- related and with unknown source in Poland (PL), Portugal (PT) and Sweden (SE), 2007-2009 (median % and 95% Credibility Interval).

	PL				PT				SE			
Source	**%**	**95% CI**		Total	**%**	**95% CI**		Total	**%**	**95% CI**		Total
Broilers	20.8	[18.8,	22.9]	21.8	40.2	[31.3,	46.9]	40.2	0.5	[0.1,	1.0]	0.5
Pigs	39.7	[36.8,	42.6]	39.8	34.2	[30.7,	37.9]	34.2	4.9	[4.0,	5.9]	4.9
Turkeys	1.0	[0.7,	1.4]	1.0	0.5	[0.0,	1.5]	0.5	1.7	[0.9,	2.6]	1.7
Layers	19.1	[16.2,	21.9]	23.8	8.1	[2.6,	17.1]	8.1	2.3	[1.1,	3.8]	2.4
Travel	0.1			0.1	0.3			0.3	77.7			77.7
Unknown	2.2	[1.2,	3.2]	2.2	10.7	[6.1,	15.2]	10.7	10.5	[9.3,	11.5]	10.5
Outbreak	17.1			11.3	6.0			6.0	2.4			2.3

Total: Includes sporadic cases and outbreak-related cases attributed to the responsible source where this was reported.

Table D8. Proportion of human *Salmonella* cases attributed to food-animal reservoirs, travel-related, outbreak- related and with unknown source in Slovenia (SI), Slovakia (SK) and the United Kingdom (UK), 2007-2009 (median %and 95% Credibility Interval).

	SI				SK				UK			
Source	**%**	**95% CI**		Total	**%**	**95% CI**		Total	**%**	**95% CI**		Total
Broilers	0.3	[0.0,	1.4]	0.3	0.0	[0.0,	0.1]	0.1	0.6	[0.4,	0.7]	0.6
Pigs	16.0	[13.6,	18.6]	16.0	17.5	[16.4,	18.6]	17.5	11.7	[10.9,	12.5]	11.7
Turkeys	3.1	[2.0,	4.4]	3.1	2.5	[2.0,	3.1]	2.5	10.1	[9.2,	11.0]	10.1
Layers	46.1	[42.9,	49.4]	47.3	74.5	[73.1,	76.1]	75.2	35.5	[34.7,	36.2]	35.5
Travel	0.0			0.0	0.8			0.8	24.3			24.3
Unknown	11.4	[8.5,	14.3]	11.4	1.7	[0.3,	3.0]	1.7	17.8	[16.9,	18.7]	17.8
Outbreak	23.1			21.9	3.0			2.3	0.0			0.0

Total: Includes sporadic cases and outbreak-related cases attributed to the responsible source where this was reported.

APPENDIX E. ESTIMATED VALUES OF POSTERIORS, *SALMONELLA* SOURCE ATTRIBUTION MODEL BY MICROBIAL SUBTYPING

E1. Estimated values for a_{cj}, source-dependent factor (median and 95% Credibility Interval)

Country	Broilers			Pigs			Turkeys			Layers		
AT	5.38E-07	[2.00E-08	2.85E-06]	4.93E-05	[4.30E-05	5.58E-05]	1.39E-04	[1.07E-04	1.76E-04]	7.42E-04	[7.14E-04	7.70E-04]
BE	2.69E-05	[2.10E-05	3.36E-05]	2.00E-04	[1.89E-04	2.11E-04]	5.27E-04	[4.54E-04	6.06E-04]	1.73E-05	[1.02E-05	2.48E-05]
CY	1.66E-06	[8.27E-07	2.74E-06]	3.51E-05	[2.93E-05	4.12E-05]	1.39E-03	[4.90E-04	2.59E-03]	1.03E-04	[4.97E-05	1.73E-04]
CZ	1.81E-06	[3.07E-07	3.86E-06]	1.41E-04	[1.30E-04	1.52E-04]	6.25E-04	[4.98E-04	7.67E-04]	8.63E-04	[8.52E-04	8.74E-04]
DE	1.11E-05	[2.36E-06	2.13E-05]	1.13E-04	[1.07E-04	1.19E-04]	1.05E-04	[8.92E-05	1.22E-04]	6.08E-04	[6.02E-04	6.15E-04]
DK	9.31E-05	[5.06E-05	1.42E-04]	2.19E-05	[1.91E-05	2.48E-05]	2.39E-03	[2.01E-03	2.79E-03]	1.08E-04	[8.54E-05	1.31E-04]
EE	7.53E-05	[1.54E-05	1.55E-04]	9.84E-05	[7.51E-05	1.24E-04]	3.43E-04	[1.27E-04	6.85E-04]	4.48E-04	[3.92E-04	5.04E-04]
ES	4.12E-08	[1.54E-09	2.18E-07]	1.07E-05	[9.91E-06	1.15E-05]	1.54E-04	[1.33E-04	1.76E-04]	1.01E-05	[9.78E-06	1.04E-05]
FI	6.27E-04	[3.15E-05	1.98E-03]	4.70E-04	[3.35E-04	5.98E-04]	2.71E-03	[7.36E-04	4.99E-03]	8.39E-06	[3.53E-06	1.34E-05]
FR	5.10E-05	[4.73E-05	5.50E-05]	3.86E-05	[3.61E-05	4.10E-05]	1.47E-04	[1.33E-04	1.62E-04]	5.99E-06	[4.65E-06	7.50E-06]
GE	6.83E-07	[2.51E-08	3.53E-06]	8.43E-06	[6.90E-06	1.01E-05]	1.07E-05	[1.51E-06	3.47E-05]	2.61E-05	[2.45E-05	2.75E-05]
HU	4.93E-06	[4.23E-06	5.67E-06]	1.06E-04	[9.72E-05	1.16E-04]	2.00E-04	[1.75E-04	2.28E-04]	2.39E-04	[2.30E-04	2.47E-04]
IE	3.39E-07	[1.83E-07	5.52E-07]	2.24E-05	[1.88E-05	2.61E-05]	2.34E-04	[1.56E-04	3.26E-04]	3.95E-05	[3.04E-05	4.91E-05]
IT	6.56E-06	[5.22E-06	8.06E-06]	5.81E-05	[5.51E-05	6.11E-05]	4.52E-05	[3.52E-05	5.72E-05]	1.34E-06	[8.14E-07	2.00E-06]
LT	2.08E-05	[7.6E-06	3.5E-05]	1.2E-04	[1.0E-04	1.4E-04]	1.3E-04	[4.6E-05	2.5E-04]	3.8E-02	[3.7E-02	3.9E-02]
LU	3.11E-05	[5.6E-06	5.2E-05]	2.8E-05	[1.2E-05	5.0E-05]	4.0E-04	[1.9E-04	6.9E-04]	6.8E-04	[5.5E-04	8.1E-04]
LV	2.85E-06	[9.1E-08	1.2E-05]	7.5E-05	[6.0E-05	9.2E-05]	7.5E-05	[3.2E-06	3.0E-04]	9.4E-05	[8.8E-05	1.0E-04]
NL	5.37E-06	[3.7E-06	6.7E-06]	2.0E-05	[1.8E-05	2.2E-05]	1.5E-04	[1.1E-04	1.8E-04]	2.9E-05	[2.6E-05	3.1E-05]

PL	2.01E-05	[	1.7E-05	,	2.0E-05	]	5.8E-05	[	5.4E-05	,	6.3E-05	]	2.1E-05	[	1.5E-05	,	2.9E-05	]	3.9E-05	[	3.4E-05	,	4.5E-05	]
PT	8.37E-06	[	6.8E+03	,	9.8E-06	]	8.2E-06	[	7.3E-06	,	9.1E-06	]	5.4E-06	[	2.9E-07	,	1.8E-05	]	2.3E-06	[	7.4E-07	,	4.9E-06	]
SE	1.46E-04	[	2.4E-05	,	2.4E-04	]	7.7E-05	[	6.3E-05	,	9.1E-05	]	5.0E-03	[	3.1E-03	,	7.1E-03	]	3.8E-04	[	2.3E-04	,	5.4E-04	]
SI	6.52E-06	[	2.2E-07	,	2.9E-05	]	1.3E-04	[	1.1E-04	,	1.5E-04	]	8.8E-05	[	5.5E-05	,	1.3E-04	]	2.3E-04	[	2.1E-04	,	2.4E-04	]
SK	1.50E-07	[	5.5E-09	,	6.6E-07	]	3.8E-04	[	3.5E-04	,	4.1E-04	]	6.4E-04	[	5.0E-04	,	8.0E-04	]	1.1E-03	[	1.0E-03	,	1.1E-03	]
UK	1.71E-06	[	1.1E-06	,	2.0E-06	]	4.4E-05	[	4.0E-05	,	4.8E-05	]	1.2E-03	[	1.1E-03	,	1.4E-03	]	4.8E-04	[	4.7E-04	,	4.9E-04	]

E2. Estimated values for q_i, *Salmonella* subtype-dependent factor (median and 95% Credibility Interval).

Serovar		95% CI	
***S.* Enteritidis**	1*		
***S.* Agona**	0.0527	[0.0488	0.0569]
***S.* Anatum**	0.0252	[0.0223	0.0283]
***S.* Bovismorbificans**	0.1854	[0.1690	0.2034]
***S.* Brænderup**	0.1386	[0.1223	0.1567]
***S.* Brandenburg**	0.1096	[0.1009	0.1190]
***S.* Bredeney**	0.0170	[0.0151	0.0191]
***S.* Derby**	0.0197	[0.0186	0.0201]
***S.* Hadar**	0.0734	[0.0670	0.0806]
***S.* Heidelberg**	0.1163	[0.0960	0.1401]
***S.* Infantis**	0.1223	[0.1167	0.1281]
***S.* Kentucky**	1.9980	[1.7970	2.2130]
***S.* Kottbus**	0.0143	[0.0124	0.0164]
***S.* Livingstone**	0.0595	[0.0540	0.0653]
***S.* London**	0.0826	[0.0751	0.0908]
***S.* Mbandaka**	0.0473	[0.0425	0.0523]
***S.* Montevideo**	0.1124	[0.1044	0.1210]
***S.* Newport**	0.2476	[0.2320	0.2645]
***S.* Rissen**	0.0302	[0.0268	0.0340]
***S.* Saintpaul**	0.0600	[0.0538	0.0671]
***S.* Typhimurium**	0.2153	[0.2054	0.2264]
***S.* Virchow**	0.2469	[0.2320	0.2625]

*The q_i value for *S.* Enteritidis was fixed to 1 meaning that all other q-values were estimated relative to this.

GLOSSARY / ABBREVIATIONS

Food-borne outbreak	Incidence, observed under given circumstances, of two or more human cases of the same disease and/or infection, or a situation in which the observed number of cases exceeds the expected number and where the cases are linked, or are probably linked, to the same food source (Directive 2003/99/EC).
Human illness source attribution	Partitioning of the human disease burden to one or more specific sources
Interquantile range	Defined as the difference between the 75^{th} and the 25^{th} percentiles, here denominated Q3 and Q1, respectively.
Median	The median of n observations is the value that divides the ordered smple into two equal pieces. Equal in the sense that the same number of observations (50%) are above and below the median value.
Points of attribution	Points in the food chain where human illness source attribution can take place, including production, distribution and consumption.
Reservoir	An animate (humans, animals, insects etc.) or inanimate object (plant, soil, etc.) or any combination of these serving as a habitat of a pathogen that produces itself in such a way as to be transmitted to a susceptible host (Pires et al., 2009).
Source	Origin of the pathogen causing infection, including reservoirs, vectors and vehicles.
Sporadic case	Case that has not been associated with known outbreaks (Engberg, 2006).